

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 18, 2002, 23:11:45 : Search time 63.6 Seconds
(without alignments)
328.331 Million cell updates/sec

Title: US-09-679-705-24
Perfect score: 987
Sequence: 1 MSLLNKIKIPFKNQAFKNGE.....AKWKEGATLAPSLDLVKRI 188

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 2: /SID55/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SID55/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SID55/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
- 5: /SID55/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
- 6: /SID55/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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- 10: /SID55/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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- 15: /SID55/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
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- 18: /SID55/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*
- 19: /SID55/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
- 20: /SID55/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
- 21: /SID55/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
- 22: /SID55/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	970.5	98.3	187	22	AAU34488
2	963.5	97.6	187	22	AAU38121
3	963.5	95.3	189	22	AAU33822
4	644.5	65.3	189	22	AAU36816
5	644.5	65.3	189	22	AAU37159
6	644.5	65.3	189	22	AAU37159
7	626	63.4	186	20	AAW30615
8	605.5	61.3	187	22	AAU36183
9	563.5	57.1	187	22	AAU34998
10	546	55.3	145	22	AAU63080
11	497.5	50.4	1873	22	ABG14982

12	370.5	37.5	271	21	AAU33833
13	370.5	37.5	271	21	AAU34590
14	370.5	37.5	273	21	AAU33832
15	370.5	37.5	273	21	AAU34590
16	351.5	35.6	266	21	AAU38191
17	350.5	35.5	199	18	AAW23715
18	346.5	35.1	224	21	AAU36959
19	346.5	35.1	256	22	AAU68037
20	343.5	34.8	198	22	AAU68036
21	335.5	34.0	219	22	ABG36215
22	334	33.8	233	21	AAU33528
23	332	33.6	206	19	AAW70222
24	328.5	33.3	220	22	ABU1843
25	324.5	32.9	198	22	AAU68040
26	323	32.7	199	18	AAU69793
27	322.5	32.7	271	18	AAU12692
28	322.5	32.7	271	21	AAU3399
29	322.5	32.7	271	22	AAU62478
30	322.5	32.7	271	22	AAU68038
31	322.5	32.7	271	22	AAU68038
32	315	31.9	199	19	AAW70221
33	307.5	31.2	263	15	AAU63754
34	306.5	31.1	196	22	ABU62769
35	304.5	30.9	178	18	AAU69794
36	299.5	30.3	242	22	ABU57947
37	295	29.9	187	19	AAU62792
38	291.5	29.5	194	19	AAU6775
39	283	28.7	194	22	ABU58322
40	283	28.7	194	22	ABU58322
41	282.5	28.6	195	22	ABU5761
42	282.5	28.6	196	22	AAU38897
43	278.5	28.2	181	14	AAU39938
44	271	27.5	193	12	AAU14303
45	264.5	26.8	195	21	AAU13470

ALIGNMENTS

RESULT 1	AAU34488	standard; Protein; 187 AA.
AC	AAU34488	
XX	14-FEB-2002	(first entry)
DE	E. coli cellular proliferation protein #69.	
XX	Antisense: prokaryotic cellular proliferation protein;	
KW	antibiotic; antibacterial; drug design.	
XX	Escherichia coli.	
OS	WO200170955-A2.	
XX	27-SEP-2001.	
XX	21-MAR-2001; 2001WO-US09180.	
PF	21-MAR-2000; 2000US-191078P.	
XX	23-MAY-2000; 2000US-206848P.	
PR	26-MAY-2000; 2000US-207727P.	
PR	23-OCT-2000; 2000US-242578P.	
PR	27-NOV-2000; 2000US-253625P.	
PR	22-DEC-2000; 2000US-257931P.	
PR	16-FEB-2001; 2001US-269308P.	
XX	(ELIT-) ELITRA PHARM INC.	
XX	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;	
PI	Yamamoto RT, Xu HH;	
XX		

Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Human prostate can
Amino acid sequenc
Amino acid sequenc
Novel human diagno
Human cancer assoc
Leishmania antigen
Drosophila melanog
Amino acid sequenc
Natural killer cel
Natural killer cel
Human natural kill
Human natural kill
Natural killer cel
Amino acid sequenc
Leishmania antigen
New flower bud ind
Drosophila melanog
Natural killer cel
Drosophila melanog
Tryparedoxin perox
Amino acid sequenc
Drosophila melanog
Drosophila melanog
Amino acid sequenc
C. pneumoniae CT60
NKEF sequence desc
M. avium av1-3 prot
C. trachomatis LGV

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DR   MPI: 2001-611495/70.
DR   N-PSDB: AAS52347..
XX   PT New polynucleotides for the identification and development of
XX   PT antibiotics, comprise sequences of antisense nucleic acids -
PS   Example 3; Seq ID No 10081; 511pp; English.
CC   The invention relates to antisense inhibitors of genes essential to
CC   prokaryotic cellular proliferation, their use in identifying the
CC   genes, their use in the discovery of novel antibiotics, the essential
CC   genes themselves and the encoded proteins. The prokaryotes used are
CC   Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC   pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC   invention is also useful for the identification of potential new targets
CC   for antibiotic development. The antisense nucleic acids can also be used
CC   to identify proteins used in proliferation, to express these proteins,
CC   and to obtain antibodies capable of binding to the expressed proteins.
CC   The proteins can be used to screen compounds in rational drug discovery
CC   programmes. The antisense nucleic acid sequence is also useful to screen
CC   for homologous nucleic acids which are required for cell proliferation in
CC   a wide variety of organisms. The present sequence represents an
CC   essential prokaryotic cellular proliferation protein.
CC   Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic
CC   format directly from WIPO at
SO   ftp.wipo.int/pub/published_pct_sequences.
XX   Sequence      187 AA;
SO   1
Query Match          98.3%; Score 970.5; DB 22; Length 187;
Best Local Similarity 99.5%; Pred. No. 3e-104;
Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1
OY    1 MSLNTRKIRPEPNQAFKNSEFIEITENKDEGRMSVFEFFYPADFTVCPTELGVDADHYE 60
DB    1 mslntnrkirpepnqafknsefieitnkdgrmsvfeffypadftvcptelgvdadye 59
OY    61 ELQKLGVDAVAVSTDTHFHFKHAKSSSETIAIKYAMIGDPTGALTRNFDNRDEGLAD 120
DB    60 elqklgvdayavstdthfhfkahwssetiakikymigdpctgaltrnfndmedeglad 119
OY    121 RATFVVDPGGIIQAIETVEFGIGROASDLIRIKAAQVYAHPGEVCPAKMKKEGATLAP 180
DB    120 ratfvvdpggiqalevtgaetigradsdlirikaagvyashnpgevcpakmkkegatlap 179
OY    181 SIDLVGKI 188
DB    180 sldlvgki 187
RESULT      2
ID AUU38121 standard; Protein; 187 AA.
AC AUU38121;
DT 14-FEB-2002 (first entry)
XX Salmonella typhi cellular proliferation protein #12.
KW Antisense; prokaryotic cellular proliferation protein;
antibiotic; antibacterial; drug design.
OS Salmonella typhi.
XX WO200170955-A2.
XX PN
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US09180.
XX
```

xx	(ELIT-) ELITRA PHARM INC.
pa	Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
pi	Yamamoto RT, Xu HH;
xx	WPI; 2001-611495/70.
dr	N-PSDB; AAS55980.
xx	New polynucleotides for the identification and development of
pt	antibiotics, comprise sequences of antisense nucleic acids -
ps	Example 3; Seq ID No 13714; 51pp; English.
xx	The invention relates to antisense inhibitors of genes essential to
cc	prokaryotic cellular proliferation, their use in identifying the
cc	genes, their use in the discovery of novel antibiotics, the essential
cc	genes themselves and the encoded proteins. The prokaryotes used are
cc	<i>Escherichia coli</i> , <i>Staphylococcus aureus</i> , <i>Salmonella typhi</i> , <i>Klebsiella</i>
cc	<i>pneumoniae</i> , <i>Pseudomonas aeruginosa</i> and <i>Enterococcus faecalis</i> . The
cc	invention is also useful for the identification of potential new targets
cc	for antibiotic development. The antisense nucleic acids can also be used
cc	to identify proteins used in proliferation, to express these proteins,
cc	and to obtain antibodies capable of binding to the expressed proteins.
cc	The proteins can be used to screen compounds in rational drug discovery
cc	programmes. The antisense nucleic acid sequence is also useful to screen
cc	for homologous nucleic acids which are required for cell proliferation in
cc	a wide variety of organisms. The present sequence represents an
cc	essential prokaryotic cellular proliferation protein.
cc	Note: The sequence data for this patent did not form part
cc	of the printed specification, but was obtained in electronic
cc	format directly from WIPO at
cc	ftp.wipo.int/pub/published_pct_sequences.
xx	Sequence 187 AA:
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Query Match	97.6%; Score 963.5; DB 22; Length 187;
Best Local Similarity	97.9%; Pred. No.2e-103;
Matches 184; Conservative 3; Mismatches 0; Indels 1; Gaps 1	
OY	1 MSLINTKIPFNQAQFKNGSEFIEITEKTDEGRMSVFEFFYPADFTFVCPTELGVDADHYE 60
Db	1 mslintkikpfknqgfkngeffievtckdegrtswsv-ffypadftfcvcltelgvdadye 59
OY	61 ELQKLGVDYVANSTDTHTFHAKMHSSSELTIAIKTKVMIDDPGALTRNDNREDEGLAD 120
Db	60 elqklgvdyvsnstldthfhkwhsssetiaktkyamldprgalrlnndmredegld 119
OY	121 RATFWVDPGGIIOALEVTAEAGIGRDSDLRLRIKAQYAASHPGCEVPAAKKKEGEATLP 180
Db	120 ratfwvdpggiilgaletaeagigrdsdlrlrikaaqyaashpgcevpakkwkegeatlp 179
OY	181 SLDLVGKI 188
Db	180 sldlvyki 187
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AAU03822	
ID	AAU03822 standard; Protein; 189 AA.
XX	AAU03822;
XX	14-FEB-2002 (first entry)
XX	

DE Staphylococcus aureus cellular proliferation protein #98.
 XX
 KW Antisense: prokaryotic cellular proliferation protein;
 XX antibiotic; antibacterial; drug design.
 OS Staphylococcus aureus.
 PN WO200170955-A2.
 XX
 XX 27-SEP-2001.
 PD
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI: 2001-611495/70.
 DR N-PSDB: AAS51681.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 5318; 511pp; English.
 XX
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 189 AA:
 SQ

Query Match 65.3%; Score 644.5; DB 22; Length 189;
 Best Local Similarity 64.2%; Pred. No. 2.1e-66;
 Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;

QY 1 MSLLTKIKPFKNQF--KNGFEITEKEDTGRMSVFFPEPADFTFCPELDGADH 58
 DB 1 msllnkelpftagaqfdpkqdkfvektgswsv-vcltpadfstvcpeleldlqng 59
 QY 59 YEELQKLGVDYAVSTDTHTFKAMHSSSETIAKRYAMIGDPTGALTFRNFMREDEGL 118
 DB 60 yeelqklgvnvtstetdthfnkawnhdsatskilytmjgpsqcltrnfnvleatgl 119
 QY 119 ADRAFFVVDPOGIIAIEVTAIGRQASDLRKIKAAQYVASHGCEVCPAWEKGEATL 178
 DB 120 agrgfllldpddgvvgaselnadqigrdastlakhikaqyrvknpgvevcapwakwegaktl 179

QY 179 APSLDLVGKI 188
 DB 180 qpgldlvvgki 189
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 AAU36816
 ID AAU36816 standard; Protein; 189 AA.
 XX
 AC AAU36816;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Staphylococcus aureus cellular proliferation protein #986.
 XX
 KW Antisense: prokaryotic cellular proliferation protein;
 KW antibiotic; antibacterial; drug design.
 OS Staphylococcus aureus.
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 PF
 XX 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI: 2001-611495/70.
 DR N-PSDB: AAS54675.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids -
 XX
 PS Example 3; Seq ID No 12409; 511pp; English.
 XX
 XX The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
 CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence represents an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 189 AA:
 SQ

Query Match 65.3%; Score 644.5; DB 22; Length 189;
 Best Local Similarity 64.2%; Pred. No. 2.1e-66;
 Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;

```

QY 1 MSLINIKIPKNOAF--KNGEFTETEDTEGRMSVFFFPADTFVCPNELGVADH 58
DB 1 mslinkeilpftaqadfpkdkqkvevgedlxgswsv-wclypadstvcpeledlqg 59
QY 59 YEELQKLGVDVAVSTDTFTFKAMHSSSETTAKIKRYAMIGPTGALTFRNFMREDDEGL 118
DB 60 yeelqklygnvsvstcdthfvkawnhdalsklytmldgdsqtltrnfdvldetlgl 119
QY 119 ADRATFVDPQGIQAIEVTAEGIGDASDLKRIKAAQYVASHPEVCPAKKKEGATL 178
DB 120 aqrgftfildpdygvaseinadigrdaslankikaagvyrknpgvecpakweegaktl 179
QY 179 APSLDLVGKI 188
DB 180 qpgldlvgki 189

RESULT 5
AAU37159
AAU37159 standard; Protein; 189 AA.
AC AAU37159;
DT 14-FEB-2002 (first entry)
DE Staphylococcus aureus cellular proliferation protein #1329.
XX
XX Antisense; prokaryotic cellular proliferation protein;
KM antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX N-PSDB; AAS55018.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3; Seq ID No 12752; 511pp; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
XX prokaryotic cellular proliferation, their use in identifying the
XX genes, their use in the discovery of novel antibiotics, the essential
XX genes themselves and the encoded proteins. The prokaryotes used are
XX Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
XX pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
XX invention is also useful for the identification of potential new targets
XX for antibiotic development. The antisense nucleic acids can also be used
XX to identify proteins used in proliferation, to express these proteins,
XX and to obtain antibodies capable of binding to the expressed proteins.
XX The proteins can be used to screen compounds in rational drug discovery
XX programmes. The antisense nucleic acid sequence is also useful to screen
XX for homologous nucleic acids which are required for cell proliferation in

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CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 189 AA:
XX
XX Query Match 65.3%; Score 644.5; DB 22; Length 189;
XX Best Local Similarity 64.2%; Pred. No. 2,1e-66;
XX Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;
XX
QY 1 MSLINIKIPKNOAF--KNGEFTETEDTEGRMSVFFFPADTFVCPNELGVADH 58
DB 1 mslinkeilpftaqadfpkdkqkvevgedlxgswsv-wclypadstvcpeledlqg 59
QY 59 YEELQKLGVDVAVSTDTFTFKAMHSSSETTAKIKRYAMIGPTGALTFRNFMREDDEGL 118
DB 60 yeelqklygnvsvstcdthfvkawnhdalsklytmldgdsqtltrnfdvldetlgl 119
QY 119 ADRATFVDPQGIQAIEVTAEGIGDASDLKRIKAAQYVASHPEVCPAKKKEGATL 178
DB 120 aqrgftfildpdygvaseinadigrdaslankikaagvyrknpgvecpakweegaktl 179
QY 179 APSLDLVGKI 188
DB 180 qpgldlvgki 189

RESULT 6
AAU37549
AAU37549 standard; Protein; 189 AA.
AC AAU37549;
DT 14-FEB-2002 (first entry)
DE Staphylococcus aureus cellular proliferation protein #1719.
XX
XX Antisense; prokaryotic cellular proliferation protein;
KM antibiotic; antibacterial; drug design.
XX
OS Staphylococcus aureus.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207727P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
XX Yamamoto RT, Xu HH;
XX WPI; 2001-611495/70.
XX N-PSDB; AAS55408.
XX
XX New polynucleotides for the identification and development of
XX antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3; Seq ID No 13142; 511pp; English.
XX

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FH	Key	Location/Qualifiers
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FT	Misc-difference	/note= "encoded by TCr
FT	Misc-difference	181
FT	Misc-difference	/note= "encoded by GTA"
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PN	JP11004690-A.	
XX		
PD	12-JAN-1999.	
XX		
XX	17-JUN-1997;	97JP-0160319.
XX		
XX	17-JUN-1997;	97JP-0160319.
PR		

PA (ELIT-)ELITRA PHARM INC.
XX
XX Haselbeck R, Ohlsen KI, Zyskind JW, Wall D, Trawick JD, Carr GJ
PI Yamamoto RT, Xu HH;
XX
DR WPI: 2001-611495/70.

Db	850	thtckawhssetiaetklyamigdptgcalttrndmmedegladretfvpdpqjiaql	909
Qy	136	EVTAEGIGRDAASDLLRKRIKAQVYASHP	163
Db	910	evtaegigrdasdlrrkikaqyashp	937
RESULT 12			
ID	AAG23833		
AC	AAG23833	standard; Protein: 271 AA.	
XX	AAG23833;		
DE	17-OCT-2000	(first entry)	
XX	Arabidopsis thaliana	protein fragment SEQ ID NO: 27285.	
XX	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter		
XX	termination sequence.		
XX	Arabidopsis thaliana.		
XX	EP1033405-A2.		
XX	06-SEP-2000.		
XX	25-FEB-2000; 2000EP-0301439.		
PR	25-FEB-1999;	99US-0121825.	
PR	05-MAR-1999;	99US-0123180.	
PR	09-MAR-1999;	99US-0123548.	
PR	23-MAR-1999;	99US-0125768.	
PR	25-MAR-1999;	99US-0126264.	
PR	29-MAR-1999;	99US-0126785.	
PR	01-APR-1999;	99US-0127462.	
PR	06-APR-1999;	99US-0128234.	
PR	08-APR-1999;	99US-0128714.	
PR	16-APR-1999;	99US-0129845.	
PR	19-APR-1999;	99US-0130077.	
PR	21-APR-1999;	99US-0130449.	
PR	23-APR-1999;	99US-0130510.	
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KW termination sequence.
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Query Match 37.5%; Score 370.5; DB 21; Length 271;
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Oy		61	ELOKIGGVNVAVSUDTFHTHKAW---HSSSETIAKIKYAMIGOPTGALTNPDMNREDEG	117
Dd		137	efekIntevlgvsdvsvfshlawqctarksgglgdlnypIvdsItksIsksfgvllIpddg	196
Oy		118	LADRATVPDQGIITIOIEVTAEGICGRDASDLRKIRKAQOVASHPCEVPAKMKEGEAT	177
Dd		197	falgIfldIdkegyIqnstlmnlngIgrsvdetmtltlqalgyqenpdvevpagwkpgeks	256
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Query Match	37.5%; Score 370.5; DB 21; Length 273;
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Best Local Similarity 38.3%; Pred. No. 2.3e-34;
Matches 70; Conservative 39; Mismatches 71; Indels 3; Gaps 1;

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GenCore version 4.5
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OM protein - protein search, using sw model

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Title: US-09-679-705-24

Perfect score: 987

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; Patent No. 574593
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; APPLICANT: Klimowski, Laura
; TITLE OF INVENTION: PARASITIC HELMINTH LARVAL THIOI SPECIFIC
; TITLE OF INVENTION: ANTIOXIDANT PROTEINS, NUCLEIC ACID MOLECULES, AND USES
; NUMBER OF INVENTIONS: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: CO
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,262
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2618-45
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 303/863-9700
; TELEFAX: 303/863-0223
; INFORMATION FOR SEQ ID NO: 2:
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-602-262-2

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RESULT 2
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Sequence 2, Application US/09004716
Patent No. 6031077
GENERAL INFORMATION:
APPLICANT: Klimowski, Laura
APPLICANT: Trapp, Cynthia A.
TITLE OF INVENTION: PARASITIC HELMINTH LARVAL SPECIFIC
TITLE OF INVENTION: ANTIOXIDANT PROTEINS, NUCLEIC ACID MOLECULES, AND USES
TITLE OF INVENTION: THERMOF
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/004,716
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,262
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-45
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-004-716-2

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; Patent No. 5985612

GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:

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: ADDRESSSEE: CAPELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
: ADDRESSSEE: STUART & OLSTEIN
: STREET: 6 Becker Farm Road
: CITY: Roseland
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
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1 MEDIUM TYPE: FLOPPY DISK
2 COMPUTER: IBM PC compatible
3 OPERATING SYSTEM: PC-DOS/MS-DOS
4 SOFTWARE: Patentin Release #1.0, Version #1.30
5 CURRENT APPLICATION DATA:
6 APPLICATION NUMBER: US/08/467,265
7 FILING DATE: 06-JUN-1995

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: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Ferraro, Gregory D.
: REGISTRATION NUMBER: 36,134
: REFERENCE/DOCKET NUMBER: 325800-456
: TELECOMMUNICATION INFORMATION:

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? TELEPHONE: 201-994-1700
?
? TELEFAX: 201-994-1744
?
? INFORMATION FOR SEQ ID NO: 15
?
? SEQUENCE CHARACTERISTICS:
?
? LENGTH: 198 amino acids
?
? TYPE: amino acid
?
? STRANDEDNESS:
?
? TOPOLOGY: linear
?
? MOLECULE TYPE: protein
?
? US-08-467-265-15

```

Query Match	34.9%;	Score 344.5;	DB 2,	Length 198;
Best Local Similarity	38.7%;	Pred. No. 1.7e-33;		
Matches 72;	Conservative 38;	Mismatches 67;	Indels 9;	Gaps 5;

OY		5	NTKI-KP--FKNOAFKNGEIEITETDEGRMSVFEFFEPADTEFVCPTELGDVAHYE	60
	:	:	: : :	:
Db		5	NARIKGAPDPKAAYVDGAKVEKYSLDYGKI-VLEFPFLDETFCPPHEIIAIFSRAE	63
	:	:	: : :	:
OY		61	ELOKLGVADVAVSTDTHTFTIKAMHSSET---IAKIKYAMI GDFGTALTNENPMRDEGS	117
	:	:	: : :	:
Db		64	DPRRIKEGEVLCSVDQSOFNHLMATINTPRKEGGLPLMIPILGGVTIRLSDEDYCVLKTDEG	123
	:	:	: : :	:
OY		118	LADRATPVDDSGOIIQAEIVABESIGDAOSLLKIKAAOVASHPBEYPAKKMGSEAT	177
	:	:	: : :	:
Db		124	IAYGGLFIIDSKGVLRQIYYNDLPFGVSUDALELVQAFOYTDBH-GEVPACPKGPSOT	182
	:	:	: : :	:

QY	178	LAPSLD	183
	:	!::!	
Db	183	IKPNVD	188

RESULT 4
US-08-467-265-15
: Sequence 15, Application US/08467265
: Patent No. 6255079
: GENERAL INFORMATION:
: APPLICANT: Ni, Jian
: Yu, Guo-Liang

APPLICANT: Ni, Jian
Yu, Guo-Liang

COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-265-16

Query Match 34.2%; Score 337.5; DB 2; Length 257;
Best Local Similarity 38.5%; Pred. No. 1.8e-32;
Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

QY 11 FKNQAFKNGEFLTEKDEGRMSVFEFFYPADFTFVCPTELGVDVADHYEELQKLGVDY 70
DB 73 FKGTAVNGEFLSLDDEKGYLV-LFFYPIDFTFVCPTEIVAFSDKANEFHDVANCEVY 131

QY 71 AVSTDHFTFKAMHSSSE---IAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVVD 127
DB 132 AVSVSHFSLAMINPRKNGGIGHNITLLSDITKQISRDYGVLSAGIALRGILFIID 191

QY 128 PGQITQAIETVTAEGIGRDSADLLRKRIKAQVYASHGECVCPAKMKEGATLAPS 181
DB 192 PNGVVKHLSVNDLPGRSVEETLRVYKAFQVETH-GEVCPANWIPESPTIRPS 244

RESULT 7
US-08-467-265-16
Sequence 16, Application US/08467265
Patent No. 6255079
GENERAL INFORMATION:
APPLICANT: NI, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-Jun-1995
CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-08-467-265-16

Query Match 34.2%; Score 337.5; DB 4; Length 257;
Best Local Similarity 38.5%; Pred. No. 1.8e-32;
Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

QY 11 FKNQAFKNGEFLTEKDEGRMSVFEFFYPADFTFVCPTELGVDVADHYEELQKLGVDY 70
DB 73 FKGTAVNGEFLSLDDEKGYLV-LFFYPIDFTFVCPTEIVAFSDKANEFHDVANCEVY 131

QY 71 AVSTDHFTFKAMHSSSE---IAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVVD 127
DB 132 AVSVSHFSLAMINPRKNGGIGHNITLLSDITKQISRDYGVLSAGIALRGILFIID 191

QY 128 PGQITQAIETVTAEGIGRDSADLLRKRIKAQVYASHGECVCPAKMKEGATLAPS 181
DB 192 PNGVVKHLSVNDLPGRSVEETLRVYKAFQVETH-GEVCPANWIPESPTIRPS 244

RESULT 8
US-09-407-891-16
Sequence 16, Application US/09407891
Patent No. 6294164
GENERAL INFORMATION:
APPLICANT: NI, Jian
Yu, Guo-Liang
Gentz, Reiner
Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/407,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,265
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-407-891-16

Query Match 34.2% Score 337.5; DB 4; Length 257;
Best Local Similarity 38.5%; Pred. No. 1.8e-32;
Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

OY 11 FKNOAKNGEIEITEKDEGRMSVFFFPYPADEFTFCVTELGADVADHEELQKLGVDY 70
DB 73 FEGTAVNGEIEKELSDPKKLYL-LFFYPLDFTFCVTELVASDKANEFHDVANCEV 131
OY 71 AVSTDTHFTKAMHSSSET--IAKIKYAMIGDPTGALTRNFMNREDEGLADRAATFVVD 127
b 132 AVSDSHFSLAMIMPRKNGSLGHMNTLLSDITKQISROYGLLESAGIALRGLEFIID 191
OY 128 PGGITQALEVTAEIGRDASDLRKIKAAQYVASHPEVCAPKMKEGEATLAPS 181
DB 192 PNGVVKHLSVNDLPVGRSVEETLRILVKAQFVETH-GEVCPANMTPEPTIKPS 244

RESULT 9

US-08-467-265-17
Sequence 17, Application US/08467265
Patent No. 5985612

GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-265-17

Query Match 33.3% Score 329; DB 2; Length 199;

Best Local Similarity 35.6%; Pred. No. 1.3e-31;
Matches 68; Conservative 43; Mismatches 70; Indels 10; Gaps 5;

OY 1 MSLINTKI-----KPRKNOA-FKNGEIEITEKDEGRMSVFFFPYPADEFTFCVTELG 55
DB 1 MSSGNKIGYPAPEKATVMPDGOFKDISLSEYKGY-VVEFFYPLDFTFCVTEIIAF 59
OY 56 ADHYEELQKLGVDYAVSDTHFTKAMHSSSET--IAKIKYAMIGDPTGALTRFNDM 112
DB 60 SDRADPEFKLNCQVIGASVDSHFCHLAWINTKKGGLGPMNPLISDPKRTIADYGL 119
OY 113 REDEGLADRAATFVVDPGITQALEVTAEIGRDASDLRKIKAAQYVASHPEVCAPKMK 172
DB 120 KADEGISFGLFLIDDKGILROITINDLPVGRSVDIIRLVQAQFTDKH-GEVCPAGMK 178
OY 173 EGEATLAPSLD 183
DB 179 PGSDTIKPDVN 189

RESULT 10

US-08-467-265-17
Sequence 17, Application US/08467265
Patent No. 6255079

GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-08-467-265-17

Query Match 33.3% Score 329; DB 4; Length 199;
Best Local Similarity 35.6%; Pred. No. 1.3e-31;
Matches 68; Conservative 43; Mismatches 70; Indels 10; Gaps 5;

OY 1 MSLINTKI-----KPRKNOA-FKNGEIEITEKDEGRMSVFFFPYPADEFTFCVTELG 55
DB 1 MSSGNKIGYPAPEKATVMPDGOFKDISLSEYKGY-VVEFFYPLDFTFCVTEIIAF 59

Sequence 14, Application US/08467265
Patent No. 5985612
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-265-14

Query Match 32.7%; Score 323; DB 2; Length 199;
Best Local Similarity 36.8%; Pred. No. 6.7e-31;
Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;
QY 1 MSLLNTKI---KPFKNOA-FKNGFEIETKDEGRMSVFFFPADFTFVCPTLGDV 55
DB 1 MSSGNKIKHPANFKATAMPDGQFKDISLDYKGY-VVFFFYPLDFTFVCPTLIIAF 59
QY 56 ADHYEELQKLVYAVSTDTHTFKAMHSSSET---IAKIKYAMIGDPTGALTRFNDM 112
DB 60 SDRAEFFKRLNCQVIGASVDSHCHLAWNTPKKGGIGPMNIPVSDPKRTIAODYGL 119
QY 113 REDEGLADRTFVVDPOGIIOALEVTAEGIGRASDLRLKRIKAOYVASHPGVCAPKWK 172
DB 120 KADEGISFRGLFIIDKGIILROITVNDPPCCRSVDETLRVQAFOTDKH-GEVCPAGWK 178
QY 173 EGEATLAPSL 182
DB 179 PGSDTIKPDV 188

RESULT 14
US-08-467-265-14
Sequence 14, Application US/08467265
Patent No. 6255079
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,265
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ferraro, Gregory D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 199 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-08-467-265-14

Query Match 32.7%; Score 323; DB 4; Length 199;
Best Local Similarity 36.8%; Pred. No. 6.7e-31;
Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;
QY 1 MSLLNTKI---KPFKNOA-FKNGFEIETKDEGRMSVFFFPADFTFVCPTLGDV 55
DB 1 MSSGNKIKHPANFKATAMPDGQFKDISLDYKGY-VVFFFYPLDFTFVCPTLIIAF 59
QY 56 ADHYEELQKLVYAVSTDTHTFKAMHSSSET---IAKIKYAMIGDPTGALTRFNDM 112
DB 60 SDRAEFFKRLNCQVIGASVDSHCHLAWNTPKKGGIGPMNIPVSDPKRTIAODYGL 119
QY 113 REDEGLADRTFVVDPOGIIOALEVTAEGIGRASDLRLKRIKAOYVASHPGVCAPKWK 172
DB 120 KADEGISFRGLFIIDKGIILROITVNDPPCCRSVDETLRVQAFOTDKH-GEVCPAGWK 178
QY 173 EGEATLAPSL 182
DB 179 PGSDTIKPDV 188

RESULT 15
US-09-407-891-14
Sequence 14, Application US/09407891
Patent No. 6294164
GENERAL INFORMATION:
APPLICANT: NI, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: NATURAL KILLER CELL ENHANCED FACTOR-C
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
ADDRESSEE: STUART & OLSTEIN
STREET: 6 Becker Farm Road

```

: CITY: Roseland
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/407,891
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/467,265
: FILING DATE: 06-JUN-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Petriato, Gregory D.
: REGISTRATION NUMBER: 36,134
: REFERENCE/DOCKET NUMBER: 325800-456
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-994-1700
: TELEFAX: 201-994-1744
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 199 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-407-891-14

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Query Match      32.7%; Score 323; DB 4; Length 199;
Best Local Similarity 36.8%; Pred. No. 6.7e-31;
Matches 70; Conservative 37; Mismatches 73; Indels 10; Gaps 5;

QY 1 MSLINTKI---KPKKQA-FKNGEPIETKDEGRMSVFEFFYPADFTFVCPTELGDV 55
DB 1 MSGGNKKIGHAPNPKATVMPDGGFKDISLSDYKGY-VFFFFYPLDFTFVCPTEIIAF 59
QY 56 ADHYEELQKLGVDYAVSTDTHTKAWHSSSET---IAKIKYAMIGDPTGALTFRNFDNM 112
DB 60 SDRAEEFKKLNCOVIGASVDSHFCFLAWNTPTKOGKGLGPMNIPLVSDPKRTIAQDYGV 119
QY 113 REDEGLADRAFTVDPQGITQAEVTAEGIGRDSPLRKIKAAQYVASHPGVCPAKMK 172
DB 120 KADEGISFGLFTLIDDKGILROITVNDPPCCRSVDETLRLVQAFQFTDKH-GEVCPAGMK 178
QY 173 EGEATLAPSL 182
DB 179 PGSDTIKPDV 188

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Search completed: May 19, 2002, 01:15:02
Job time: 7152 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 19, 2002, 00:29:30 ; Search time 51.62 Seconds

(without alignments)
349.957 Million cell updates/sec

Title: US-09-679-705-24

Perfect score: 987

Sequence: 1 MSLLNTKIRKPFKNQAFKNGE.....AKWKEGPAFLAPSLDVGKI 188

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	970.5	98.3	187	2	JN0289 alkyl hydroperoxid
2	970.5	98.3	187	2	D90709 alkyl hydroperoxid
3	970.5	98.3	187	2	H85559 alkyl hydroperoxid
4	963.5	97.6	187	2	D80577 alkyl hydroperoxid
5	742.5	75.2	187	2	D87610 alkyl hydroperoxid
6	714	72.3	206	2	G82668 subunit C of alkyl
7	677.5	68.6	187	2	F65883 alkyl hydroperoxid
8	644.5	65.3	189	2	F69804 alkyl hydroperoxid
9	624.5	63.3	168	2	PS0179 hypochlorite prote
10	622.5	63.1	184	1	A35441 alkyl hydroperoxid
11	612.5	62.1	179	2	S52934 alkyl hydroperoxid
12	605.5	61.3	187	2	C83627 alkyl hydroperoxid
13	603.5	61.1	187	2	A86667 alkyl hydroperoxid
14	488.5	49.5	188	2	D71314 probable alkyl hyd
15	455.5	46.1	211	2	G70343 alkyl hydroperoxid
16	365	36.7	242	2	S49173 hypochlorite prote
17	362	36.0	210	2	T06318 thiol-specific ant
18	361	35.9	265	2	T09211 thiol-specific ant
19	354	35.9	198	2	T09211 thiol-specific ant
20	344.5	34.9	198	2	T09211 thiol-specific ant
21	338	34.2	199	2	I52425 probable thioredox
22	337.5	34.2	257	2	U00064 MEK3 protein - mou
23	334	33.8	199	2	A46711 probable thioredox
24	334	33.4	576	2	T16005 hypochlorite prote
25	330	33.4	203	2	A12385 peroxiredoxin (imp
26	329.5	33.4	200	2	I51016 peroxiredoxin asso
27	329	33.3	199	2	A48513 macropinase 23k str
28	324.5	32.9	195	2	UC2258 substrate protein
29	322.5	32.7	271	2	G01790 probable thiol-spe

30	319.5	32.4	183	2	A83983 2-cys peroxiredoxi
31	312	31.6	199	2	S73193 hypochlorite prote
32	312	31.6	226	2	S43598 mer5 homolog R07E5
33	311	31.5	200	2	AB0388 probable alkyl hyd
34	307	31.1	200	2	S76284 hypochlorite prote
35	306.5	31.1	180	2	B69867 2-cys peroxiredoxi
36	306	31.0	192	2	T41413 thioleoxin peroxi
37	302	30.6	200	2	AB0552 probable peroxidas
38	300	30.4	200	2	G83204 probable peroxidas
39	288	29.2	207	2	E82287 antioxiidant, Ahpc/
40	283.5	28.7	195	2	A43858 alkyl hydroperoxid
41	282.5	28.6	196	2	H86587 thio-specific anti
42	282.5	28.6	196	2	E72036 thio-specific anti
43	280	28.4	199	2	F83540 probable alkyl hyd
44	276	28.0	195	2	E87164 alkyl hydroperoxid
45	266	27.0	181	2	AD1275 2-cys peroxiredoxi

ALIGNMENTS

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RESULT 1
JN0289
alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - Escherichia coli
N:Alternate names: sulfate starvation-induced protein SS18
C:Species: Escherichia coli
C>Date: 16-Sep-1992 #sequence revision 30-Sep-1997 #text_change 11-Jun-1999
C:Accession: C64794; JN0289; S78624
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: C64794
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-187 <BLAT>
A:Cross-references: GB:AE000166; GB:U00096; NID:91786819; PIDN:AC73706.1; PID:917868
A:Experimental source: strain K-12, substrain MG1655
R:Ueshima, R.; Fujita, N.; Ishihama, A.
Biochem. Biophys. Res. Commun. 184, 634-639, 1992
A:Title: Identification of Escherichia coli proteins cross-reacting with antibodies a
A:Reference number: JN0286; MUID:92246944
A:Accession: JN0289
A:Molecule type: protein
A:Residues: 2-31 <UES>
A>Note: This protein fragment has exact coincidence, except Ile-24, with the first 31
R:Quadrini, M.; Staudenmann, W.; Kertesz, M.; James, P.
Eur. J. Biochem. 239, 773-781, 1996
A:Title: Analysis of global responses by protein and peptide fingerprinting of proteol.
A:Reference number: S78617; MUID:96370830
A:Accession: S78624
A:Molecule type: protein
A:Residues: 2-11 <QUA>
A:Genetics:
A:Gene: ahpc
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
C:Keywords: oxidoreductase
F:2-187/Product: alkyl hydroperoxidase reductase c22 protein #status experimental <MAY>
F:11-146/Domin: alkyl hydroperoxidase c22 protein homology <C22>

Query Match 98.3% Score 970.5; DB 2; Length 187;
Best Local Similarity 99.5% Pred. No. 3e-81; 0; Indels 1; Gaps 1;
Matches 187; Conservative 0; Mismatches 0;

OY 1 MSLLNTKIRKPFKNQAFKNGEFLTEKDEGRSVFFFPADFTFVCPTELGADVADHE 60
DB 1 MSLLNTKIRKPFKNQAFKNGEFLTEKDEGRSVFFFPADFTFVCPTELGADVADHE 59
OY 61 ELQKLGVDVAVSTDTHTTHKAMHSSSEFTIAIKYAMIGDPTGALTRFNNRREDGLAD 120

```

Db 60 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 119
QY 121 RATEFVDPGGIIQALIEVTAEGIGRSDSLRLKRIKAQYVAASHPEVCAPKMKEGEATLAP 180
Db 120 RATEFVDPGGIIQALIEVTAEGIGRSDSLRLKRIKAQYVAASHPEVCAPKMKEGEATLAP 179
QY 181 SLDLVGKI 188
Db 180 SLDLVGKI 187

RESULT 2
D90709
alkyl hydroperoxide reductase C22 subunit [imported] - Escherichia coli (strain 0157:H7,
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: D90709
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C. G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shingawa, H.
NA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <HAY>
A:Cross-References: GB:BA000007; PIDN:BA034067.1; PID:g13360102; GSPDB:GN00154
A:Experimental source: strain 0157:H7, substrain RMD 0509952
C:Genetics:
A:Gene: ECS0644
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 98.3%; Score 970.5; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;
Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSLINIKIRPFKNQAKNKEFEITEKDEGRMSVFFFPADFTFVCPTELGVDADHYE 60
Db 1 MSLINIKIRPFKNQAKNKEFEITEKDEGRMSV-FFFPADFTFVCPTELGVDADHYE 59
QY 61 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 120
Db 60 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 119
QY 121 RATEFVDPGGIIQALIEVTAEGIGRSDSLRLKRIKAQYVAASHPEVCAPKMKEGEATLAP 180
Db 120 RATEFVDPGGIIQALIEVTAEGIGRSDSLRLKRIKAQYVAASHPEVCAPKMKEGEATLAP 179
QY 181 SLDLVGKI 188
Db 180 SLDLVGKI 187

RESULT 3
H85359
alkyl hydroperoxide reductase (EC 1.6.4.-) c22 protein - Escherichia coli (strain 0157:H
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 31-Dec-2001
C:Accession: H85359
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85359
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <STO>
A:Cross-References: GB:AE005174; NID:g12513501; PIDN:AGS4940.1; GSPDB:GN00145; UMGF:207
C:Genetics:
A:Experimental source: strain 0157:H7, substrain EDL933
A:Gene: ahpc

C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p
C:Keywords: oxidoreductase

Query Match 98.3%; Score 970.5; DB 2; Length 187;
Best Local Similarity 99.5%; Pred. No. 3e-81; Mismatches 0; Indels 1; Gaps 1;
Matches 187; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSLINIKIRPFKNQAKNKEFEITEKDEGRMSVFFFPADFTFVCPTELGVDADHYE 60
Db 1 MSLINIKIRPFKNQAKNKEFEITEKDEGRMSV-FFFPADFTFVCPTELGVDADHYE 59
QY 61 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 120
Db 60 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 119
QY 121 RATEFVDPGGIIQALIEVTAEGIGRSDSLRLKRIKAQYVAASHPEVCAPKMKEGEATLAP 180
Db 120 RATEFVDPGGIIQALIEVTAEGIGRSDSLRLKRIKAQYVAASHPEVCAPKMKEGEATLAP 179
QY 181 SLDLVGKI 188
Db 180 SLDLVGKI 187

RESULT 4
AB0577
alkyl hydroperoxide reductase c22 protein [imported] - Salmonella enterica subsp. ent
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: This species has also been called Salmonella typhi
A:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AB0577
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Mout, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Park, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
A:Reference number: AB0502; PMID:11677608
A:Accession: AB0577
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <PAR>
A:Cross-References: GB:AL513382; PIDN:CAD05084.1; PID:g16501859; GSPDB:GN00176
C:Genetics:
A:Gene: STY0653
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 p

Query Match 97.6%; Score 963.5; DB 2; Length 187;
Best Local Similarity 97.9%; Pred. No. 1.3e-80; Mismatches 3; Indels 1; Gaps 1;
Matches 184; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSLINIKIRPFKNQAKNKEFEITEKDEGRMSVFFFPADFTFVCPTELGVDADHYE 60
Db 1 MSLINIKIRPFKNQAKNKEFEITEKDEGRMSV-FFFPADFTFVCPTELGVDADHYE 59
QY 61 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 120
Db 60 ELQKLGVDYAVSTDTHTFHAKAMHSSSETIAIKYAMIGDPGALTRNFDNKRDEGLAD 119
QY 121 RATEFVDPGGIIQALIEVTAEGIGRSDSLRLKRIKAQYVAASHPEVCAPKMKEGEATLAP 180
Db 120 RATEFVDPGGIIQALIEVTAEGIGRSDSLRLKRIKAQYVAASHPEVCAPKMKEGEATLAP 179
QY 181 SLDLVGKI 188
Db 180 SLDLVGKI 187

RESULT 5
D87610
alkyl hydroperoxide reductase, subunit c [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: D87610
R:McNern, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Debey, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, M.J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87610
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-187 <STO>
C:Cross-references: GB:AE005673; NID:913424540; PIDN:AAK24880.1; GSPDB:GN00148
C:Gene: CC2918
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 75.2% Score 742.5; DB 2; Length 187;
Best Local Similarity 72.3% Pred. No. 2e-60;
Matches 136; Conservative 27; Mismatches 24; Indels 1; Gaps 1;

OY 1 MSLLNTKIKPKRNOAKFKGEFLEITEKDEGRMSVSEFFEFYADFTFVCPTELSGVADHYE 60
Db 1 MSLLNTKIKPKPTAQAQKDGKFEVYSEADVKGMSV-FFEFYADFTFVCPTELELDADYD 59
61 ELQKLGVDVYAVSTDTHTFTHKAMHSSSETIAKIKAMIGDPTGALTNRFDNMREDEGLAD 120
Db 60 VETRLGVEIVAVSDTHTSHKAMHSSPAIGKIKITWGDPSGOVTNNFELMRPGVGLAD 119
OY 121 RATEVVDPOGIIQAEVTAEGIGRDSPLLRKIKAAQYVAHPGCEVPAKKEGEATLAP 180
Db 120 RGTFLVDDQGYIOEFAVTEAGIGRNALIELLRKIKAAQYVAHPGCEVPAKKEGEKTLP 179
OY 181 SLIDVIGKI 188
Db 180 SLIDVIGKI 187

RESULT 6
G82668
Subunit C of alkyl hydroperoxide reductase XF1530 [Imported] - Xylella fastidiosa (strain
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: G82668
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: G82668
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-206 <STN>
A:Cross-references: GB:AE003983; GB:AE003849; NID:99106567; PIDN:AAF84339.1; GSPDB:GN001
R:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facinola, A.P.; Ferreira, A.J.S.
Submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laig
Chado, M.A.; Medeira, A.M.B.N.; Medeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, F
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
C:Gene: XF1530

C:superfamily: alkyl hydroperoxide reductase C22 protein, alkyl hydroperoxidase C22

```
Query Match          72.3%, Score 714; DB 2; Length 206;
Best Local Similarity 69.1%, Pred. No. 8,9e-58;
Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;

OY 1 MSLNTRKIPKRNQAFKNGEFLIEETKDEGRMWSYFFFFYPADFTFCPTELGDVADHYE 60
    |||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
DB 21 MSLNTEILISFKATYVKKNGOFEVSEAVLKGMWV-FVFFYADFTFCPTELDEDLADHYE 79
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
OY 61 ELQKGVGVYVASTPTHTHTHKAMSSSETIKIKYAMIGDPGALTFRNDMREDEGLAD 120
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
DB 80 ELQKGVGVYVSTDIHTSHKAMHDISAIGIKIKYAMIGDPGHTHSRNF-NVLRPSGLAD 138
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
OY 121 RATEFVDDPGIIQIAETVAEGIGRDPASDLRKIKAAQVYASHPGECAPAKKKEGATLAP 180
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
DB 139 RGTFLIDPGVAYQSVETIAEIGGRAPKELLRKVAKAIYVANHPPGVCPAKKDEGGKTLAP 198
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
OY 181 SLDLVGKI 188
    |||:||||:
DB 199 SLDLVGKI 206

RESULT 7
FE9583
alkyl hydroperoxide reductase (EC 1.6.4.-) small chain - Bacillus subtilis
N:Alternate names: 54K protein; alkyl hydroperoxide reductase chain C22 homolog; NADH
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: FE9583; G44519
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ben
C.; Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gal
lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinio
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portec
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadleir, Y.; Sato, T.; Scanl
A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se
danchin, M.; Tamakoshi, A.; Tanaka, T.; Terpetra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, M.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zunsstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; MUID:98044033
A:Accession: FE9583
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-187 <KUN>
A:Cross-references: GB:Z99124; GB:AL009126; NID:g2636442; PIDN:CAB16046.1; PID:g26365
A:Experimental source: strain 168
R:DOWDS, B.C.A.
submitted to the Protein Sequence Database, February 1993
A:Reference number: A44519
A:Accession: G44519
A:Molecule type: protein
A:Residues: 2-36, 'XX', 39-41 <DOM>
C:Genetics:
A:Gene: ahpc
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase C22 p
C:Keywords: NAD; oxidoreductase
F:2-187/Product: alkyl hydroperoxide reductase small chain #status predicted <MA>
F:11-144/Domain: alkyl hydroperoxidase c22 protein homology <C22>

Query Match          68.6%, Score 677.5; DB 2; Length 187;
Best Local Similarity 64.9%, Pred. No. 1,7e-54;
Matches 122; Conservative 32; Mismatches 33; Indels 1; Gaps 1;

OY 1 MSLNTRKIPKRNQAFKNGEFLIEETKDEGRMWSYFFFFYPADFTFCPTELGDVADHYE 60
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
DB 21 MSLNTEILISFKATYVKKNGOFEVSEAVLKGMWV-FVFFYADFTFCPTELDEDLADHYE 79
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
OY 61 ELQKGVGVYVASTPTHTHTHKAMSSSETIKIKYAMIGDPGALTFRNDMREDEGLAD 120
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
DB 80 ELQKGVGVYVSTDIHTSHKAMHDISAIGIKIKYAMIGDPGHTHSRNF-NVLRPSGLAD 138
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
OY 121 RATEFVDDPGIIQIAETVAEGIGRDPASDLRKIKAAQVYASHPGECAPAKKKEGATLAP 180
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
DB 139 RGTFLIDPGVAYQSVETIAEIGGRAPKELLRKVAKAIYVANHPPGVCPAKKDEGGKTLAP 198
    |||:||||:||||:||||:||||: |||:||||:||||: |||:||||:||||: |||:||||:||||:
OY 181 SLDLVGKI 188
    |||:||||:
DB 199 SLDLVGKI 206
```

Db 1 MSLSGKEVLPEEAKFKNGEFIDVTNEDLKGOMSV-FCFYADSFVCPTELEDJQOEYX 59
Oy 61 ELQKIGVDYAVSTDTHEFTTKRAMHSSSETIAIKIKYAMTGDPTGALTIRNFNDNMREDEGLAD 120
 |::|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 60 ALKEGVSEVSYSSTDTHFVKHGMDHSSEKISKITYAMTGDSQTISRNPDLDETETIAD 119
 |||||
Oy 121 RATEVVDFOGIIQAIEVAEGISGRDASDLLRKRIKAQYVAHPGCVPAAKKGEGETALP 180
 ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 120 RGTFFIIDPDGYIVQEINAGSIGRDAENLVNKRAAQIVRONPGFEVCAPAKEBGGETTITP 179
 |||||
Oy 181 SLIDLVGKI 188
 ||::|::|
Db 180 SLDLVGI 187
 |||||

RE**S**U**L**T 8
F89804 alkyl hydroperoxide reductase subunit C [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
Accession: F89804
Kuroud, M.; Oht, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogucma, A.; Mizutani-Oi, Y.; Kodayashii, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A>Title: Whole genome sequencing of methicillin-resistant staphylococcus aureus.
A:Reference number: AB9758; MUUD:21311952; PMID:11418146
A:Accession: F89804
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1189 <CUR>
A:Cross-references: GB:BA000018; PID:g13700295; PIDN:BAB41593.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: ahpc
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase c22 prot

Query Match 65.3%; Score 644.5; DB 2; Length 189;
Best Local Similarity 64.2%; Pred. No. 1.8e-51;
Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2;

Oy 1 MSIINTKIKPPKNAAF--KNGEFITEKTOTRGMRNVFPFFYPADFCTPCTELGDVADH 58
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 1 MSLLKELLPFTAQAFDPKKDKQKFVEIQEDLKGSNS-VCTTPADFSVCPTELEDDONQ 59
 |||||

Oy 59 YEEOKLIGVDYAVASTDTHTFHTRKAMHSSSETIAKTIKYAMDGPTGALTIRNFNDNMREDEGL 118
 |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
 60 YEEOKLIGVNVSSTDTHTFHFAKHWDSDAISKITTYMIGDSPQGITIRNFDVIDEANGCL 119
 |||||

Oy 119 ADRAFVFVDPOGIIQAIENVTAEGISGRDASDLLRTKKAQYVASHPGEVCPAAKKMEGETLT 178
 ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 120 AORGFIFIIDPVGOVQASEINADGISGRDASTLAHKIKAQYVRKNGEVCPAAKWEGCACTL 179
 |||||

Oy 179 APSLDLVGI 188
 |::::|
Db 180 QPSLDLVGI 189
 |||||

RE**S**U**L**T 9
PSO179 hypothetical protein (nhd 5' region) - Bacillus sp. (fragment)
C:Species: Bacillus sp.
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
Accession: PSO179
Fu,Xu, X.; Koyana, N.; Cui, M.; Yamagishi, A.; Nosoh, Y.; Oshima, T.
J. Biochem. 109, 678-683, 1991
A>Title: Nucleotide sequence of the gene encoding NADH dehydrogenase from an alkalophile
A:Reference number: JX0166; MUUD:92011449
A:Accession: PSO179
A:Molecule type: DNA
A:Residues: 1-168 <XUX>
A:Experimental source: strain YN-1

C:Superfamily: alkyl hydroperoxide reductase C22 protein, alkyl hydroperoxidase C22 p
F:1-130/Domain: alkyl hydroperoxidase C22 protein homology (fragment) <C22>

```
Query Match          63.3%; Score 624.5; DB 2; Length 168;
Best Local Similarity 67.5%; Pred. No. 1e-49;
Matches 114; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

OY 20 EFETTEKDTGRMSVFFEFYPADTFEVCPTELGDVDADHYEELQKLGVDVAVSTDTHT 79
      |||||::: :|||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1 EFIEVSESEFGQMSV-LCFYPADTFEVCPTLELDIQEYALKELGVEFASSTDTHFT 59

OY 80 HKAMSSSETIAKIKYAMIGDPTGALTFRNPNMDEDESLARATFVDPQIIAIEVTA 139
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 60 HKGWDSEETIGKITYAMIGDPSQTLRNPNFVLEVSALDRGFIIIDPDGVQAAEINA 119

OY 140 EIGRDAEDLLRKIKAAQYVASHPEVCPRAKKEGATLAPSLDVGKI 188
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 120 EIGRDAESTLVNKKIAAQYVRNPNPEVCPRAKQESDETLKFSLDLVGKI 168

RESULT 10
A35441
alkyl hydroperoxide reductase (EC 1.6.-.-) C22 protein - Salmonella typhimurium
C:Species: Salmonella typhimurium
C:Date: 07-Sep-1990 #sequence.revision 18-Nov-1994 #text.change 19-Oct-1995
C:Accession: A35441; S07525
R:Ratagila, L.A.; Storz, G.; Brodsky, M.H.; Lal, A.; Ames, B.N.
J. Biol. Chem. 265, 10535-10540, 1990
A>Title: Alkyl hydroperoxide reductase from Salmonella typhimurium. Sequence and homo
A:Reference number: A35441; MUID:90285183
A:Accession: A35441
A:Molecule type: DNA
A:Residues: 1-184 <TAR>
A:Cross-references: GB:J05478
A>Note: the nucleotide sequence given is inconsistent with Genbank accession J05478
R:Ratagila, L.A.; Storz, G.; Ames, B.N.
J. Mol. Biol. 210, 709-719, 1989
A>Title: Identification and molecular analysis of oxyr-regulated promoters important
A:Reference number: S07525; MUID:90135925
A:Accession: S07525
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-21 <TA2>
A>Note: part of this sequence, including the amino end of the mature protein, was con
C:Genetics:
A:Gene: ahpc
A:Map position: 13 min
C:Function:
A:Description: noncatalytic component of the active enzyme, which protects the cell a
C:Superfamily: alkyl hydroperoxide reductase C22 protein; alkyl hydroperoxidase C22 p
C:Keywords: oxidoreductase
F:11-146/Domain: alkyl hydroperoxidase C22 protein homology <C22>

Query Match          63.1%; Score 622.5; DB 1; Length 184;
Best Local Similarity 97.5%; Pred. No. 1.7e-49;
Matches 117; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 MSLITKTRPKRNOAFKNGFEIETTEKDTBGRMSVFFEFYPADTFVCPPELDGVADHYE 60
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 1 MSLITKTRPKRNOAFKNGFEIETTEKDTBGRMSV-FFEFYPADTFVCPPELDGVADHYE 59

OY 61 ELQKGVGVAVASTDTHTHKAMSSSETIAKIKYAMIGDPTGALTFRNPNMREDEGLAD 120
      |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db 60 ELQKGVGVAVSYDTHHTHKAMSSSETIAKIKYAMIGDPTGALTFRNPNMREDEGLAD 119

RESULT 11
S52934
alkyl hydroperoxide reductase (EC 1.6.4.-) C22 protein - Staphylococcus aureus (fragm
C:Species: Staphylococcus aureus
C:Date: 06-Jun-1995 #sequence.revision 22-May-1998 #text.change 17-Jul-1998
```

Matches	93;	Conservative	32;	Mismatches	61;	Indels	1;	Gaps	1;
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 19, 2002, 00:31:21 ; Search time 40.11 Seconds

(without alignments)
181,483 Million cell updates/sec

Title: US-09-679-705-24

Perfect score: 987
Sequence: 1 MSLMTKIRPFKNQAFKNKE.....AKKKEGATLAPSLDVCKI 188

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

otal number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	965.5	97.8	186	1	AHPC_ECOLI
2	958.5	97.1	186	1	AHPC_SALTY
3	677.5	68.6	187	1	AHPC_BACSU
4	624.5	63.3	168	1	YNDH_BACSP
5	366.5	37.1	266	1	BAS1_ARATH
6	362	36.7	210	1	BAS1_WHEAT
7	361	36.6	198	1	PDX2_RAT
8	361	36.6	210	1	BAS1_HORVU
9	358.5	36.3	198	1	PDX2_MOUSE
10	354	35.9	265	1	BAS1_SPIOL
11	346.5	35.1	256	1	PDX3_HUMAN
12	343.5	34.8	199	1	PDX2_HUMAN
13	338	34.2	198	1	PDX1_RAT
14	337.5	34.2	257	1	PDX3_MOUSE
15	335.5	34.0	257	1	PDX3_BOVIN
16	334	33.8	199	1	PDX1_HUMAN
17	330.5	33.5	199	1	TDX2_BRUMA
18	329.5	33.4	200	1	TDX1_CINPY
19	329	33.3	199	1	PDX1_MOUSE
20	322.5	32.7	271	1	PDX4_HUMAN
21	322	32.6	229	1	TDX1_BRUMA
22	321.5	32.6	274	1	PDX4_MOUSE
23	312	31.6	199	1	YC42_PORPU
24	312	31.6	226	1	TDX1_CAREL
25	307	31.1	200	1	Y755_SYNY3
26	305.5	31.0	199	1	TDX1_TRYBR
27	291.5	29.5	194	1	TDX1_FASHE
28	291	29.5	200	1	TDX1_ONCMY
29	285.5	28.9	233	1	TSAL_CANAL
30	265	27.0	178	1	CR29_ENTHI
31	265.5	26.9	178	1	R20K_CLOPA
32	262	26.5	204	1	YC42_ODOSI
33	258.5	26.2	195	1	YSA2_YEAST

34	250.5	25.4	195	1	TSAL_YEAST
35	249.5	25.3	197	1	YSA2_BUCAI
36	243.5	24.7	127	1	PDX2_PIG
37	241	24.4	198	1	TSAL_HELPJ
38	241	24.4	198	1	TSAL_HELPJ
39	226.5	22.9	215	1	TDXH_HELPJ
40	226.5	22.9	215	1	TDXH_HELPJ
41	223	22.6	216	1	TDXH_HELPJ
42	221	22.4	216	1	TDXH_HELPJ
43	220.5	22.3	215	1	TDX1_HELPJ
44	216.5	21.9	215	1	TDXH_HELPJ
45	216.5	21.9	217	1	TDXH_HELPJ

ALIGNMENTS

RESULT	ID	Sequence	Standard	PRT	AA
1	AHPC_ECOLI	US-09-679-705-24	US-09-679-705-24	186	AA
AC	P26427	01-AUG-1992 (Rel. 23, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-) (SCRP-23)				
DE	(Sulfate starvation-induced protein 8) (SS18)				
GN	AHPC OR B0605 OR Z0749 OR EC50644				
OS	Escherichia coli, and				
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;				
OC	Escherichia				
OX	NCBI_TaxID=562, 83334;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12;				
RC	MEDLINE=92276370; PubMed=1592833;				
RX	Smillie D.A., Hayward R.S., Suzuki T., Fujita N., Ishihama A.;				
RT	"Locations of genes encoding alkyl hydroperoxide reductase on the				
RT	physical map of the Escherichia coli K-12 genome.";				
RL	J. Bacteriol. 174:3826-3827(1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12 / MG1655;				
RC	MEDLINE=97426617; PubMed=9278503;				
RX	Blaetter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.;				
RA	Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.;				
RA	Gregor J., Davis N.W., Kirkpatrick J.A., Goeden M.A., Rose D.J.;				
RA	Mau B., Shao Y.;				
RT	"The complete genome sequence of Escherichia coli K-12.";				
RL	Science 277:1453-1474(1997).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.;				
RA	Federlespiel N., Hyman R., Kaiman S., Komp C., Kurd O., Lew H., Lin D.;				
RA	Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;				
RL	Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=K12;				
RC	MEDLINE=97061202; PubMed=8905232;				
RX	Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.;				
RA	Ikeno K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.;				
RA	Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.;				
RA	Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.;				
RA	Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.;				
RT	"A 718-kb DNA sequence of the Escherichia coli K-12 genome				
RT	corresponding to the 12.7-28.0 min region on the linkage map.";				
RL	DNA Res. 3:137-155(1996).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=O157:H7 / EDL933 / ATCC 700927;				
RC	MEDLINE=21074935; PubMed=11206551;				

RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mawhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamosis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.,
RT "Genome sequence of enterohaemorrhagic *Escherichia coli* O157:H7.",
RL Nature 409:529-533(2001).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN-O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Hida T., Takami H., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.,
RT "Complete genome sequence of enterohaemorrhagic *Escherichia coli*
RT O157:H7 and genomic comparison with a laboratory strain K-12.",
RL DNA Res. 8:11-22(2001).
[7]
RP SEQUENCE OF 1-30.
RC MEDLINE=92246944; PubMed=1575737;
RA Ueshima R., Fujita N., Ishihama A.;
RT "Identification of *Escherichia coli* proteins cross-reacting with
RT antibodies against region 2.2 peptide of RNA polymerase sigma
RT subunit.",
RL Biochem. Biophys. Res. Commun. 184:634-639(1992).
[8]
RP SEQUENCE OF 1-13.
RC STRAIN-K12 / W3110;
RA Pasquali C., Sanchez J.-C., Xavier F., Golaz O., Hughes G.J.,
RA Fruhlinger S., Paquet N., Wilkins M., Appel R.D., Bairoch A.,
RL Hochstrasser D.F.,
RT Submitted (SEP-1994) to the SWISS-PROT data bank.
[9]
RP SEQUENCE OF 1-27 AND 69-80.
RC STRAIN-K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.,
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of *Escherichia coli* K-12.",
RL Electrophoresis 18:1259-1313(1997).
[10]
RP SEQUENCE OF 1-20.
RC STRAIN-K12;
RX MEDLINE=96081923; PubMed=7499381;
RA Cha M.-K., Kim H.-K., Kim I.-H.,
RT "Thioredoxin-linked 'thiol peroxidase' from periplasmic space of
RT *Escherichia coli*.",
RL J. Biol. Chem. 270:28635-28641(1995).
[11]
RP SEQUENCE OF 1-10.
RC STRAIN-K12 / MC4100;
RX MEDLINE=96370830; PubMed=8774726;
RA Quadroni M., Staudenmann W., Kertesz M., James P.,
RT "Analysis of global responses by protein and peptide fingerprinting
RT of proteins isolated by two-dimensional gel electrophoresis.
RT Application to the sulfate-starvation response of *Escherichia coli*.",
RL Eur. J. Biochem. 239:773-781(1996).
[12]
RP FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED
CC DITHIOL FORM.
[13]
RP SUBUNIT: HOMODIMER (BY SIMILARITY).
[14]
RP -1- PTM: THE CYS-46-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-46 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-165-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTRAMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
CC BY THIOREDOXIN.
[15]
RP -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
[16]
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CC -----
DR EMBL: D13187; BAA02485.1; -
DR EMBL: AE000166; AAC73706.1; -
DR EMBL: 082598; AAB40806.1; -
DR EMBL: D90702; AAB35244.1; -
DR EMBL: D90701; BAA35235.1; -
DR EMBL: AE005240; AAG54940.1; -
DR EMBL: AP002552; BAB34067.1; -
DR PIR: JN0289; JN0289.
DR HSSP: P30041; 1PRX.
DR SWISS-2DPAGE: P26427; COLI.
DR ECODBASE: B020.9; 6TH EDITION.
DR Ecogene: EGI1384; ahpc.
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
KW Oxidoreductase; Complete proteome.
FT INIT_MET 0 0
FT ACT_SITE 46 46 BY SIMILARITY.
FT ACT_SITE 165 165 BY SIMILARITY.
SQ SEQUENCE 186 AA; 20630 MW; 40CDA2D344CA196B CRC64;

Query Match 97.8%; Score 965.5; DB 1; Length 186;
Best Local Similarity 99.5%; Pred. No. 7.9e-80;
Matches 186; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 SLINTKIRKPKKNAFNGEPIETETKOTEGRMSVFEFFYPADTFPCPELGDVAHYEE 61
DB 1 SLINTKIRKPKKNAFNGEPIETETKOTEGRMSVFEFFYPADTFPCPELGDVAHYEE 59
QY 62 LOKLGVAVYAVSDTHFTFKAMHSSETIAKIKYAMIGPTGALTFNPNMREDEGLADR 121
DB 60 LOKLGVAVYAVSDTHFTFKAMHSSETIAKIKYAMIGPTGALTFNPNMREDEGLADR 119
QY 122 AFNVDPGGIIOAIEVTAIGRDSADLRLKIKAAQYVASHPEVCAPAKWKEGEATLAPS 181
DB 120 AFNVDPGGIIOAIEVTAIGRDSADLRLKIKAAQYVASHPEVCAPAKWKEGEATLAPS 179
QY 182 LDLVCKI 188
DB 180 LDLVCKI 186

RESULT 2
AHPC_SALTY STANDARD; PRT; 186 AA.
ID AHPC_SALTY
AC P19479;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ALKYL hydroperoxide reductase C22 protein (EC 1.6.4.-).
GN AHPC OR STM0608 OR STY0653.
OS *Salmonella typhimurium*, and
OC *Salmonella typhimurium*.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC *Salmonella*.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S. typhimurium; STRAIN-TN1379;
RX MEDLINE=90285183; PubMed=2191951;
RA Tarrapija L.A., Storz G., Brodsky M.H., Lai A., Ames B.N.,
RT "Alkyl hydroperoxide reductase from *Salmonella typhimurium*. Sequence
RT and homology to chlorodoxin reductase and other flavoprotein
RT disulfide oxidoreductases.",
RL J. Biol. Chem. 265:10535-10540(1990).
[2]
RP REVISIONS TO C-TERMINUS.
RC SPECIES-S. typhimurium;
RX MEDLINE=94316629; PubMed=8041738;

RA Chae H.Z., Robison K., Poole L.B., Church G., Storz G., Rhee S.G.;
 RT "Cloning and sequencing of thiol-specific antioxidant from mammalian
 RT brain: alkyl hydroperoxide reductase and thiol-specific antioxidant
 RT define a large family of antioxidant enzymes.";
 RT Proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC MEDLINE-21534948; PubMed-11677609; / SCS1412 / ATCC 700720;
 RX McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., All J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Milvane E.,
 RA Waterston R., Wilson R.K.;
 RA "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 RT LT2.";
 RN Nature 413:852-856(2001).
 RL [4]
 RP SEQUENCE OF 1-20 FROM N.A.
 RC SPECIES-S. typhimurium;
 RX MEDLINE-90133925; PubMed-2693740;
 RA Tartaglia L.A., Storz G., Ames B.N.;
 RT "Identification and molecular analysis of oxyR-regulated promoters
 RT important for the bacterial adaptation to oxidative stress.";
 RT J. Mol. Biol. 210:709-719(1989).
 RN [5]
 RP SEQUENCE OF 1-24.
 RC SPECIES-S. typhimurium; STRAIN-OXYR1;
 RX MEDLINE-89109157; PubMed-2643600;
 RA Jacobson F.S., Morgan R.W., Christman M.F., Ames B.N.;
 RT "An alkyl hydroperoxide reductase from *Salmonella typhimurium*
 RT involved in the defense of DNA against oxidative damage. Purification
 RT and properties.";
 RT J. Biol. Chem. 264:1488-1496(1989).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S. typhimurium; STRAIN-CT18;
 RX MEDLINE-21534947; PubMed-11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltham T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagsels K.,
 RA Krogh A., Larsen T.S., Leathers S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT *enterica* serovar Typhimurium CT18.";
 RT Nature 413:848-852(2001).
 CC -1- FUNCTION: DIRECTLY REDUCES ALKYL HYDROPEROXIDES WITH THE USE OF
 CC ELECTRON DONATED BY THE 57 KDA FLAVOPROTEIN ALKYL HYDROPEROXIDE
 CC REDUCTASE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- PTM: THE CYS-46-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H₂O₂, AND THE OXIDIZED CYS-46 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-165-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
 CC BY THIOREDOXIN.
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC -----
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 CC -----
 DR EMBL: J05473; AAA16431.1; -;
 DR EMBL: AE008724; AAL19559.1; -;
 DR EMBL: AL627267; CAD05084.1; -;
 DR PIR: A35441; A35441.
 DR PIR: S07525; S07525.

DR HSP: P30041; 1PRX.
 DR Styene: SG10004; ahpc.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Oxidoreductase; Complete proteome.
 FT INIT MET 0
 FT ACT SITE 46 46 BY SIMILARITY.
 FT ACT SITE 165 165 BY SIMILARITY.
 FT CONFLICT 1 1 S -> G (IN REF. 5).
 FT CONFLICT 4 4 N -> D (IN REF. 5).
 FT CONFLICT 13 13 Q -> N (IN REF. 5).
 FT CONFLICT 16 16 K -> H (IN REF. 5).
 FT CONFLICT 19 19 E -> H (IN REF. 5).
 FT CONFLICT 22 22 E -> S (IN REF. 5).
 SQ SEQUENCE 186 AA; 20616 MW; 83D48A7A667F5DB0 CRC64;
 Query Match 97.1%; Score 958.5; DB 1; Length 186;
 Best Local Similarity 97.9%; Pred. No. 3.4e-79;
 Matches 183; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
 QY 2 SLINIKIKPFKNQARKNGFEIITEKDTGRNSVFFFPADFTYCPTELDVADHYE 61
 DB 1 SLINIKIKPFKNQARKNGFEIITEKDTGRNSV-FFFPADFTYCPTELDVADHYE 59
 QY 62 LKLGVDYAVSTDPFTHKAMHSSEITAKIKYAMIGPTGALTFPNMREDEGLAR 121
 DB 60 LKLGVDYAVSTDPFTHKAMHSSEITAKIKYAMIGPTGALTFPNMREDEGLAR 119
 QY 122 ATEFVDPQIGIAIEVTAEGIGRSDLLRKIKAAQYVAHSGEVCAPAKWKEGATLAD 181
 DB 120 ATEFVDPQIGIAIEVTAEGIGRSDLLRKIKAAQYVAHSGEVCAPAKWKEGATLAD 179
 QY 182 LDLYGKI 188
 DB 180 LDLYGKI 186
 RESULT 3
 AHPC_BACSU STANDARD; PRT; 187 AA.
 ID AHPC_BACSU P53562;
 AC P80239; P53562;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alkyl hydroperoxide reductase C22 protein (EC 1.6.4.-) (General stress
 DE protein 22).
 GN AHPC.
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; *Bacillus*/Clostridium group;
 OC *Bacillus*/Staphylococcus group; *Bacillus*.
 OX NCBI_Taxid=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168;
 RA Kashara Y., Nakai S., Yoshikawa H., Ogasawara N.;
 RL Submitted (NOV-1995) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 1-41.
 RC STRAIN-168 / YB886;
 RX MEDLINE-94236234; PubMed-8180695;
 RA Hartford O.M., Dows B.C.A.;
 RT "Isolation and characterization of a hydrogen peroxide resistant
 RT mutant of *Bacillus subtilis*.";
 RT Microbiology 140:297-304(1994).
 RN [3]
 RP SEQUENCE OF 1-14.
 RC STRAIN-IS58;
 RX MEDLINE-94282319; PubMed-8012595;
 RA Voelker U., Engelmann S., Maul B., Rietdorf S., Voelker A.,
 RA Schmidt R., Mach H., Hecker M.;
 RT "Analysis of the induction of general stress proteins of *Bacillus*
 RT *subtilis*.";

```

RL Microbiology 140:741-752(1994).
CC -1- FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED
CC DIHIOI FORM.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS AND
CC GLUCOSE LIMITATION.
CC -1- PTM: THE CYS-47-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-47 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-166-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
CC BY THIOREDOXIN.
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC -----
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CC -----
DR EMBL: D78193; BAA11268.1; -
DR EMBL: 299124; CAB16046.1; -
DR Subtilist; BG11385; ahpc.
DR Interpro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
DR Oxidoreductase; Heat shock; Complete proteome.
DR ACT_SITE 47 47 BY SIMILARITY.
FT ACT_SITE 166 166 MISSING (IN REF. 3).
FT CONFLICT 2 2 V->VV (IN REF. 3).
FT CONFLICT 8 8
SQ SEQUENCE 187 AA; 20627 MW; 10DF6643BC90F54E CRC64;

```

Query Match 68.6%; Score 677.5; DB 1; Length 187;
 Best Local Similarity 64.9%; Pred. No. 5.9e-54;
 Matches 122; Conservative 32; Mismatches 33; Indels 1; Gaps 1;

```

QY 1 MSLLINKIPFNQAFKNGEFTETKEDGRMSVFEFFYPADFTFCVCTELGADVADHYE 60
DB 1 MSLLINKIPFNQAFKNGEFTETKEDGRMSVFEFFYPADFTFCVCTELGADVADHYE 59
QY 61 ELQKLGADVAVYVSTDTHTFHAKMHSSSETIAKIKYAMIDPGALTRFNDNREDEGLAD 120
DB 60 AKEKLGVEYVSVSTDTHTFHAKMHSSSETIAKIKYAMIDPGALTRFNDNREDEGLAD 119
QY 121 RAFFVVDPOGIIQALEVTETEGIGRSDSLRKIKAAQYVASHGFCVCPAKKKEGATLAP 180
DB 120 RCTFIIDPGVAYQYVEINAGIGRSDSLRKIKAAQYVASHGFCVCPAKKKEGATLAP 179
QY 181 SLDLVGKI 188
DB 180 SLDLVGKI 187

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RESULT 4
 YNDH_BACSP STANDARD: PRT; 168 AA.
 AC P26830;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein in NDH 5' region (Fragment).
 OS Bacillus sp. (strain YN-1).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_Taxid=1409;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92011449; PubMed=1917890;
 RA Xu X., Koyama N., Cui M., Yamagishi A., Nosoh Y., Oshima T.;
 RT "Nucleotide sequence of the gene encoding NADH dehydrogenase from an
 alkalophilic, Bacillus sp. strain YN-1.";

```

RL J. Biochem. 109:678-683(1991).
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- PTM: THE CYS-28-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-28 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-147-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE IS SUBSEQUENTLY REDUCED
CC BY THIOREDOXIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D10701; BAA01544.1; -
DR PIR: PS0179; PS0179.
DR Interpro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA; 1.
DR Hypothetical protein; Antioxidant.
DR NON_TER 1 1 BY SIMILARITY.
FT ACT_SITE 28 28 BY SIMILARITY.
FT ACT_SITE 147 147 MISSING (IN REF. 3).
SQ SEQUENCE 168 AA; 18479 MW; 2D58C57B87726CDE CRC64;

```

Query Match 63.3%; Score 624.5; DB 1; Length 168;
 Best Local Similarity 67.5%; Pred. No. 3e-49;
 Matches 114; Conservative 25; Mismatches 29; Indels 1; Gaps 1;

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QY 20 EFLEIETKDEGRMSVFEFFYPADFTFCVCTELGADVADHYEELQKLGADVAVSTDTHT 79
DB 1 EFLEIETKDEGRMSVFEFFYPADFTFCVCTELGADVADHYEELQKLGADVAVSTDTHT 59
QY 80 HKAMHSSSETIAKIKYAMIDPGALTRFNDNREDEGLADRAATVVPQGIQALEVYA 139
DB 60 HKGMHSSSETIAKIKYAMIDPGALTRFNDNREDEGLADRAATVVPQGIQALEVYA 119
QY 140 EIGIRASDLKIKAAQYVASHGFCVCPAKKKEGATLAPSLDLVGI 188
DB 120 EIGIRASDLKIKAAQYVASHGFCVCPAKKKEGATLAPSLDLVGI 168

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RESULT 5
 BASI_ARATH STANDARD: PRT; 266 AA.
 AC Q96291; P92938; Q957Y0;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 2-cys peroxidoredoxin BAS1, chloroplast precursor.
 GN BAS1 OR AT3G11630 OR T19F11.3 OR F24K9.28.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Baler M., Dietz K.-J.;
 RT "2-Cys peroxidoredoxin bas1 from Arabidopsis thaliana.";
 RL (in) Plant Gene Register PGR96-031.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=97408940; PubMed=9263459;
 RA Baler M., Dietz K.-J.;
 RT "The plant 2-cys peroxidoredoxin BAS1 is a nuclear-encoded chloroplast
 protein: its expressional regulation, phylogenetic origin, and
 implications for its specific physiological function in plants.";

RL Plant J. 12:179-190(1997).
 [3]
 RP REVISIONS.
 RA Baier M.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoorge W., Unselid M.,
 RA Farman B., Valle G., Bloeker H., Perez-Alonso M., Odenaier B.,
 RA DeSény M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
 RA De Simone V., Choise N., Artiguenave F., Robert C., Brothier P.,
 RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Queller F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
 RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezel A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
 RA Condat A., Hornischer K., Kauer G., Loehner T., H. Nordstiek G.,
 RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
 RA Cooke R., Lande M., Berger-Liauro C., Purnelle B., Masuy D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Aguilou A., Flores M., Liguori R., Vitale D.,
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
 RA Cressy T.H., Haas B., Malt R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltischer J., Sellers P., Gill J.E., Feldlyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
 RA Matanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana."
 RL Nature 408:820-822(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Chen H., Johnson-Hopson C., Khan S., Shinn P.,
 RA Ecker J.;
 RT "Full length cDNA sequence of Arabidopsis thaliana."
 RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IN THE
 CC DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF. INVOLVED IN THE
 CC DETOXIFICATION OF ALKYL HYDROPEROXIDES. EXPRESSION IS RERESSED IN
 CC RESPONSE TO A HIGHLY REDUCED CELLULAR THIOL POOL, AND SLIGHTLY
 CC INDUCED BY OXIDATIVE STRESS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- PTM: THE CYS-119-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O(2), AND THE OXIDIZED CYS-119 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-241-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDUXIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC
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 CC
 CC EMBL: X94218; CAA63909.1; -
 DR EMBL: Y10478; CAA71503.1; -
 DR EMBL: X97910; CAA66484.2; -
 DR EMBL: AC009918; AAF02131.1; -
 DR EMBL: AC008153; AAG51430.1; -
 DR EMBL: AF324996; AAG40348.1; -
 DR HSSP: P30041; IPRX.

DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Chloroplast; Transf. peptide.
 FT TRANSIT 1 65 CHLOROPLAST (BY SIMILARITY).
 FT CHAIN 66 266
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT ACT_SITE 241 241 BY SIMILARITY.
 FT CONFLICT 101 101 E -> K (IN REF. 1).
 FT CONFLICT 101 101 I -> N (IN REF. 1 AND 2).
 FT CONFLICT 122 122 MISSING (IN REF. 1).
 FT CONFLICT 192 192 I -> IGI (IN REF. 2).
 FT CONFLICT 233 235 IOE -> TG (IN REF. 1).
 FT CONFLICT 247 247 P -> S (IN REF. 1).
 SQ SEQUENCE 266 AA; 29092 MW; 2CEB476A1A8694AD CRC64;
 Query Match 37.1%; Score 366.5; DB 1; Length 266;
 Best Local Similarity 37.7%; Pred. No. 7.7e-26;
 Matches 69; Conservative 39; Mismatches 72; Indels 3; Gaps 1;
 QY 1 MSLLNKIRPKRQAKRNGEFTETKDPTEGRKSVFFFPADPTVCPELGDVADHYE 60
 DB 72 LPLVGNKAPDEEAEVDFEFIKVLSYVILFFPLDFTVCPEITAFSDRHS 131
 QY 61 ELQKLGVDVYASTDFTHTKAN---HSSSETAKIKYAMIGDPGALTFRNPMREDEG 117
 DB 132 EFKLNTVEVLGVSVDVFSHLAWQDRKSGGLDNLPLSDVTSISKSFVLHDOG 191
 QY 118 LADRAFTVVDPGIIOAIEVTAEGIRGDSDLRKIKAAQVASHPGENCPRKKEGEAT 177
 DB 192 IALRGFLIDKEGVIOHSTINNGIRSVDETMRITQALQYIQENPDVCPAGMKRGEKS 251
 QY 178 LAP 180
 DB 252 MKP 254
 RESULT 6
 BASL_WHEAT STANDARD; PRT; 210 AA.
 ID BASL_WHEAT
 AC P80602;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 2-cys peroxidexin BASL, chloroplast precursor (Thiol-specific
 DE antioxidant protein) (Fragment).
 GN TSA.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 OX [1]
 RP SEQUENCE FROM N.A.
 RP STRAIN=CV. NORIN 61; TISSUE=Seedling;
 RA Tsunoyama Y., Toyoshima Y.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 11-35.
 RC STRAIN=CV. NOURIN 61; TISSUE=Leaf;
 RA Tsunoyama Y., Takashi S., Toyoshima Y.;
 RL Submitted (MAY-1996) to the SWISS-PROT data bank.
 CC -1- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IN THE
 CC DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- PTM: THE CYS-64-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O(2), AND THE OXIDIZED CYS-64 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-185-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDUXIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.

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DR EMBL: AB000405; BAA19099.1; -
 DR HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Antioxidant; Chloroplast; Transit peptide.
 FT TRANSIT 1 10 CHLOROPLAST.
 FT NON_TER 1 1
 FT CHAIN 11 210 2-CYS PEROXIREDOXIN BAS1.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 185 185 BY SIMILARITY.
 FT ACT_SITE 210 AA; 23326 MW; E2D488179D6937E6 CRC64;
 SQ SEQUENCE

Query Match 36.7%; Score 362; DB 1; Length 210;
 Best Local Similarity 38.3%; Pred. No. 1.5e-25;
 Matches 70; Conservative 37; Mismatches 72; Indels 4; Gaps 2;

QY 1 MSLLNTKIPKFNQAEKEFEITEKDEGRMSVFEFFYPADTFVCPTELGVDADHYE 60
 DB 17 LPLVGNKADPFAAEVDFDEINVKLSIDYIGKKYVLFEPDFTFVCPTEIATFSDRHE 76
 QY 61 ELQKLGVDYAVSTDPHFHKAM---HSSSETIAKIKYAMIGDPGALTRFNDNREDEG 117
 DB 77 EEKINTEELGVSVSFSLHAWGVTERKSGGLGDKYPLVSDYVSKISKSEFVLIPDGG 136
 QY 118 LADRAFVVDPOGIIQAEIVTAEGIGRDSLLRKIKAAQYVAHSHPGECAPAKKGEAT 177
 DB 137 IALRGFLIIRKGVIOHSHIINNLGIGRSYDELRTLRALQYV-KRDEVCPAGKKGES 195
 QY 178 LAP 180
 DB 196 MKP 198

RESULT 7
 PDX2_RAT
 ID PDX2_RAT STANDARD; PRT; 198 AA.
 AC P35704;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 40, Last annotation update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT Peroxiredoxin 2 (Thioredoxin peroxidase 1) (Thioredoxin-dependent
 DT peroxide reductase 1) (Thiol-specific antioxidant protein) (TSA).
 DT PRDX2 OR TDPX1.
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94316629; PubMed=8041738;
 RA Chae H.Z., Robinson K., Poole L.B., Church G., Storz G., Rhee S.G.;
 RA "Cloning and sequencing of thiol-specific antioxidant from mammalian
 RA brain: alkyl hydroperoxide reductase and thiol-specific antioxidant
 RA define a large family of antioxidant enzymes.";
 RA Proc. Natl. Acad. Sci. U.S.A. 91:7017-7021(1994).
 CC -!- FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED
 CC THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE
 CC ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN
 CC ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT
 CC PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR
 CC NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR
 CC CONCENTRATIONS OF H(2)O(2).
 CC -!- SUBUNIT: HOMODIMER; DISULFIDE-LINKED. UPON OXIDATION (BY

CC SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- PTM: THE CYS-51-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O(2), AND THE OXIDIZED CYS-51 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-172-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC
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DR EMBL: U06099; AAA19959.1; -
 DR HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Antioxidant.
 FT ACT_SITE 51 51 BY SIMILARITY.
 FT ACT_SITE 172 172 BY SIMILARITY.
 FT ACT_SITE 198 AA; 21784 MW; FC6AD9B0E9C4447B CRC64;
 SQ SEQUENCE

Query Match 36.6%; Score 361; DB 1; Length 198;
 Best Local Similarity 40.3%; Pred. No. 1.7e-25;
 Matches 73; Conservative 35; Mismatches 65; Indels 8; Gaps 4;

QY 9 KP---FKNOAFKNGEITEKDEGRMSVFEFFYPADTFVCPTELGVDADHYEELQTL 65
 DB 10 KRAPDPTGAIVADVADGAKKEIKLSIDYIGKKYVLFEPDFTFVCPTEIATFSDRHE 68
 QY 66 GVDYAVSTDPHFHKAMHSSSET---IAKIKYAMIGDPGALTRFNDNREDEGLADRA 122
 DB 69 GCEVLGVSVDQSOTHLAWINTPRKEGLGPLNPLADVTYKLSQNYGVAKNDEGLAYNG 128
 QY 123 TFWVDPOGIIQAEIVTAEGIGRDSLLRKIKAAQYVAHSHPGECAPAKKGEATLAPSL 182
 DB 129 LPLVGNKADPFAAEVDFDEINVKLSIDYIGKKYVLFEPDFTFVCPTEIATFSDRHE 187
 QY 183 D 183
 DB 188 D 188

RESULT 8
 BAS1_HORVU
 ID BAS1_HORVU STANDARD; PRT; 210 AA.
 AC Q96468;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DT 2-cys peroxiredoxin BAS1, chloroplast precursor (thiol-specific
 DT antioxidant protein) (Fragment).
 GN Hordeum vulgare (Barley).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. GERBEL; TISSUE=leaf;
 RX MEDLINE=96382424; PubMed=8790288;
 RA Balier M., Dietz K.-U.;
 RA "Primary structure and expression of plant homologues of animal and
 RA fungal thioredoxin-dependent peroxide reductases and bacterial alkyl
 RA hydroperoxide reductases.";
 RA Plant Mol. Biol. 31:553-564(1996).
 CC -!- FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IMPORTANT IN

CC THE DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF.
 CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Chloroplast (By similarity).
 CC -1 TISSUE SPECIFICITY: EXPRESSED IN LEAF BLADE, SHEATH, BASTIPLAST,
 CC STEM AND GREEN SPIKE. MAXIMAL EXPRESSION IN YOUNG DEVELOPING
 CC SHOOT SEGMENTS WHERE CELL DIVISION AND ELONGATION TAKE PLACE. NOT
 CC EXPRESSED IN ROOTS.
 CC -1 DEVELOPMENTAL STAGE: MAXIMAL LEVELS ARE SEEN IN 4-DAY OLD
 CC SEEDLINGS AND DECLINE DURING AGING OF THE SEEDLING.
 CC -1 PTM: THE CYS-64-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O(2), AND THE OXIDIZED CYS-64 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-185-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -1 SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC -----
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 CC -----
 CC EMBL: Z34917; CAA84396.1; -.
 CC HSSP: P30041; 1PRX.
 CC InterPro: IPR000866; Ahpc-TSA.
 CC Pfam: PF00578; Ahpc-TSA; 1.
 CC Antioxidant; Chloroplast; Transit peptide.
 CC NON_TER 1
 CC TRANSIT 1
 CC CHAIN <1 10 CHLOROPLAST (BY SIMILARITY).
 CC FT 11 210 2-CYS PEROXIREDOXIN BAS1.
 CC ACT_SITE 64 64 BY SIMILARITY.
 CC FT 185 185 BY SIMILARITY.
 CC ACT_SITE 210 AA; 4DD488179D6BCAC9 CRC64;
 CC SEQUENCE

Query Match 36.6%; Score 361; DB 1; Length 210;
 Best Local Similarity 38.3%; Pred. No. 1.8e-25;
 Matches 70; Conservative 37; Mismatches 72; Indels 4; Gaps 2;

OY 1 MSLINTKIKPFKNQAFKNGEFTETKDEGRMSVFFFPADFTVCPTGLGVADHYE 60
 DB 17 LPLVNKAAPDAFAAEVDFEDFNKLSIDYIKKKYVLFPPIDFTFCPTETIAFSDRB 76
 OY 61 ELQKGVAVYANSTDTHTFKAW---HSSEFTIAKKYAMIGDPGALTRNDNMREDG 117
 DB 77 EEEKINTELGVSDVSFVSHLAWOTERKSGGLGDKYPLVDVTKSISKSGVLIPDGG 136
 OY 118 LADRAFTFVVDPGIIOAIEVTAEGIGRDASDLRLKIKAKOYVASHGEGCPAKWKGEAT 177
 DB 137 IALRGLFIIDKRGVIOHSTINNLGIGRSDVETLRLOALQY-KPDEVCPAGWKGEKS 195
 OY 178 LAP 180
 DB 196 MKP 198

RESULT 9
 PDX2_MOUSE STANDARD: PRT; 198 AA.
 AC Q61171; Q60796;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Peroxiredoxin 2 (Thioredoxin peroxidase 1) (Thioredoxin-dependent
 DE peroxidase reductase 1) (Thiol-specific antioxidant protein) (TSA).
 GN PRDX2 OR TDPX1 OR TPX.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Brain;
 RX MEDLINE-97238626; PubMed-9115640;
 RA Ichimaya S., Davis J.G., O'Rourke D.M., Katsumata M., Greene M.I.;
 RT "Murine thioredoxin peroxidase delays neuronal apoptosis and is
 RT expressed in areas of the brain most susceptible to hypoxic and is
 RT ischemic injury.";
 RL DNA Cell Biol. 16:311-321(1997).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN-129;
 RA Oberbauer I.;
 RL Submitted (SEP-1996) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6;
 RA Chae H.-Z., Kim H., Rhee S.;
 RL Submitted (JUL-1995) to the EMBL/Genbank/DBJ databases.
 CC -1 FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED
 CC THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE
 CC ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN
 CC ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT
 CC PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR
 CC NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR
 CC CONCENTRATIONS OF H(2)O(2).
 CC -1 SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY
 CC SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1 TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN BONE
 CC MARROW. HIGH LEVELS ALSO FOUND IN HEART, BRAIN, KIDNEY AND
 CC SKELETAL MUSCLE. LOWER LEVELS IN LIVER, LUNG AND THYMUS.
 CC -1 PTM: THE CYS-51-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O(2), AND THE OXIDIZED CYS-51 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-172-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
 CC -1 SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U51679; AAB01941.1; -.
 CC DR EMBL: X82067; CAA57566.1; -.
 CC DR EMBL: U20611; AAA69475.1; -.
 CC DR HSSP: P30041; 1PRX.
 CC DR SMIS-2DPAGE; 061171; MOUSE.
 CC MGD; MGI:109486; Prdx2.
 CC InterPro: IPR000866; Ahpc-TSA.
 CC DR Pfam: PF00578; Ahpc-TSA; 1.
 CC KW Antioxidant.
 CC FT ACT_SITE 51 51 BY SIMILARITY.
 CC FT ACT_SITE 172 172 G -> A (IN REF. 3).
 CC FT CONFLICT 97 97
 CC FT CONFLICT 182 182 T -> N (IN REF. 3).
 CC FT SEQUENCE 198 AA; 21778 MM; FE216F5426F7174D CRC64;
 CC SEQUENCE

Query Match 36.3%; Score 358.5; DB 1; Length 198;
 Best Local Similarity 40.3%; Pred. No. 2.8e-25;
 Matches 71; Conservative 35; Mismatches 65; Indels 5; Gaps 3;

OY 11 FKNQAFKNGEFTETKDEGRMSVFFFPADFTVCPTGLGVADHYEELQKGVAVY 70
 DB 15 FATAVADGAFKIKLSVDYRGKY-VLFFPYPLDFTFCPTETIAFSDHADDFKLGCEVL 73
 OY 71 AVSTDTHTFKAWHSSSE---IAKKYAMIGDPGALTRNDNMREDGLADRAFTVVD 127
 DB 74 GVSVDQFTHLAWINTPRREGIGLPIPLADVTKSLSQNGVGLKNDEGIAYRGLFIID 133

OY 128 PGGIIAIEVTAEGIGRDASDLRKIKAAQYVASHPEGCVPAMKKEATLAPSD 183
 DB 134 AKGVLAQITVNDLPVGRSVDEALRLVQAFQYTDH-GEVCPAGMKRPSDTIKPVD 188

RESULT 10
 BASI_SPIOI STANDARD: PRT: 265 AA.

AC 024364:
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 2-CYS peroxiredoxin BASI, chloroplast precursor (Thiol-specific
 DE antioxidant protein).

GN BASI.
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 NCBI_TaxID=3562;

RP SEQUENCE FROM N.A.
 RC STRAIN=CV. GERBEL; TISSUE=Leaf;
 RX MEDLINE=96382424; PubMed=8790288;
 RA Balier M., Dietz K.-J.;

RT "Primary structure and expression of plant homologues of animal and
 RT fungal thioredoxin-dependent peroxidase reductases and bacterial alkyl
 RT hydroperoxide reductases";
 RL Plant Mol. Biol. 31:553-564(1996).

CC - FUNCTION: MAY BE AN ANTIOXIDANT ENZYME PARTICULARLY IN THE
 CC DEVELOPING SHOOT AND PHOTOSYNTHESIZING LEAF.

CC - SUBUNIT: HOMODIMER (BY SIMILARITY).

CC - SUBCELLULAR LOCATION: Chloroplast (BY SIMILARITY).

CC - PTM: THE CYS-119-SH GROUP IS THE PRIMARY SITE OF
 CC RAPIDLY REACTS WITH CYS-240-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDUXIN (BY SIMILARITY).

CC - SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC -----

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DR EMBL; X94219; CA663910.1; -
 DR HSSP; P30041; IPRX.

DR InterPro: IPR000866; Ahpc-TSA.

DR Pfam: PF00578; Ahpc-TSA; 1.

KW Antioxidant; Chloroplast; Transit peptide.

FT TRANSIT 1 65 CHLOROPLAST (BY SIMILARITY).

FT CHAIN 66 265 2-CYS PEROXIREDOXIN BASI.

FT ACT_SITE 119 119 BY SIMILARITY.

FT ACT_SITE 240 240 BY SIMILARITY.

SO SEQUENCE 265 AA; 28895 MW; 11F479093C2F573B CRC64;

Query Match 35.9%; Score 354; DB 1; Length 265;
 Best Local Similarity 37.7%; Pred. No. 1e-24;
 Matches 69; Conservative 38; Mismatches 72; Indels 4; Gaps 2;

OY 1 MSINTKIPFNQAKNCEFEITEKTEGRMSVEFFFPADFTVCPTLGDVADHYE 60
 DB 72 LPLVGNKADDFEAEVDFDEFFIKVKYILFFYPIDFTFCPTETIAFSDRS 131

OY 61 ELQKLGVDVYAVSTDFHFKAM---HSSSEFIARKIYAMIGDPALTRNDPMKEDGG 117
 DB 132 EEKLTLETVGVSVDSFSLHAWQTRKSGGLGDLNPLYSIVTKSISKSEGLVLIHDOG 191

OY 118 LADRAFPVDPGGIIAIEVTAEGIGRDASDLRKIKAAQYVASHPEGCVPAMKKEGAT 177
 DB 192 IALRGFLIIDEKGVIGHQSTNNIGIGRSVDETRKTLQALQY-IGNPEVCPAMKKEGERS 250

OY 178 LAP 180
 DB 251 MKP 253

RESULT 11
 PDX3_HUMAN

ID PDX3_HUMAN STANDARD: PRT: 256 AA.

AC P30048; P35690; Q13776;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Thioedoxin-dependent peroxidase reductase, mitochondrial precursor
 DE (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (MER3 protein
 DE homolog) (HBC189) (PRX III).

GN PRDX3 OR AOP1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

OC NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=95251598; PubMed=7733872;

RA Tsui K., Copeland N.G., Jenkins N.A., Olinata M.,
 RA Mammalian antioxidant protein complements alkylhydroperoxide
 RT reductase (ahpc) mutation in Escherichia coli.";

RT Biochem. J. 307:377-381(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 148-240 FROM N.A.

RX MEDLINE=94108427; PubMed=7506601;

RA Takeda J., Yano H., Eng S., Zeng Y., Bell G.I.;

RA "A molecular inventory of human pancreatic islets: sequence analysis
 RT of 1000 cDNA clones.";

RL Hum. Mol. Genet. 2:1793-1798(1993).

RN [4]

RP SEQUENCE OF 63-72.

RC TISSUE=Liver;

RX MEDLINE=93162045; PubMed=1286669;

RA Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,

RA Appel R.D., Hughes G.J.;

RT "Human liver protein map: a reference database established by
 RT microsequencing and gel comparison.";

RL Electrophoresis 13:992-1001(1992).

CC - FUNCTION: THIOREDUXIN-DEPENDENT PEROXIDE REDUCTASE. PROTECTS
 CC RADICAL-SENSITIVE ENZYMES FROM OXIDATIVE DAMAGE BY A RADICAL-
 CC GENERATING SYSTEM.

CC - SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY
 CC SIMILARITY).

CC - SUBCELLULAR LOCATION: Mitochondrial.

CC - PTM: THE CYS-108-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
 CC H(2)O(2), AND THE OXIDIZED CYS-108 (PROBABLY CYS-SOH) RAPIDLY
 CC REACTS WITH CYS-229-SH OF THE OTHER SUBUNIT TO FORM AN
 CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
 CC REDUCED BY THIOREDUXIN (BY SIMILARITY).

CC - SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
 CC -----

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CC  -----
CC  EMBL: D49396; BA08389.1;
DR  EMBL: BC002685; AA02685.1;
DR  EMBL: T10952; NOT_ANNOTATED_CDS.
DR  HSSP: P30041; IPRX.
DR  SWISS-2DPAGE: P30048; HUMAN.
DR  Sienna-2DPAGE: P30048;
DR  MIM: 604769;
DR  InterPro: IPR000866; Ahpc-TSA.
DR  Pfam: PF00578; Ahpc-TSA.1.
KW  Antioxidant; Mitochondrion; Transit peptide.
FT  TRANSIT 1 62 MITOCHONDRION.
FT  CHAIN 63 256 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
FT  ACT_SITE 108 108 BY SIMILARITY.
FT  ACT_SITE 229 229 BY SIMILARITY.
SQ  SEQUENCE 256 AA; 27692 MW; 8BBB7F5E5BFE9BE CRC64;

Query Match 35.1%; Score 346.5; DB 1; Length 256;
Best Local Similarity 40.2%; Pred. No. 4.6e-24;
Matches 70; Conservative 33; Mismatches 66; Indels 5; Gaps 3;

OY 11 FKNQAFKNGEFTETKTEKGRMSVFFFPADFTFCPTLEGDVADHYEELQKLGVDY 70
DB 72 FKGTAIVNGEFDLSDPKKYL-LFFYPLDFTFCPTLEIVASDKANEFHDVNCVY 130
OY 71 AVSTDTHTTKAMHSSSET---IAKIKAMICDPGALTRNDNMREDEGLADRAFFVVD 127
DB 131 AVSVSHSHSLAMINTPRKNGIGLHMNTALSDLTQISRDYGLLEGSGALRGLEIID 190
OY 128 PGQIIQAEVTEAGIGRSDSLRRKIKAAQVASHPEGVCPRKWEGETLAPS 181
DB 191 PNGVILKHSVNDLPVGRSVYEETRLVKAFQYETH-GEVCPANMTPDSETPKS 243

RESULT 12
PDX2_HUMAN STANDARD: PRT: 198 AA.
ID P32119; P35701; P31945; Q92763;
AC P32119; P35701; P31945; Q92763;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peroxisome oxidin 2 (Thioredoxin peroxidase 1) (Thioredoxin-dependent
DE peroxidase reductase 1) (Thiol-specific antioxidant protein) (TSA) (PRP)
DE (Natural killer cell enhancing factor B) (NKEF-B).
GN PRDX2 OR TDPX1 OR NKEFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE-94193012; PubMed-814038;
RX Lim Y.-S., Cha M.-K., Kim H.-K., Kim I.-H.;
RT "Type thiol-specific antioxidant protein from human brain: gene
RT cloning and analysis of conserved cysteine regions.";
RL Gene 140:279-284(1994).
RN [2]
RN SEQUENCE FROM N.A.
RP MEDLINE-9429283; PubMed-8026862;
RX Shau H., Butterfield L.H., Chiu R., Kim A.;
RT "Cloning and sequence analysis of candidate human natural killer-
RT enhancing factor genes.";
RL Immunogenetics 40:129-134(1994).
RN [3]
RN SEQUENCE OF 35-198 FROM N.A.
RP Oberbauer I.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE OF 17-25; 140-150 AND 163-185.
RC TISSUE=Keratinocytes;

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RX MEDLINE-93162043; PubMed-1286667;
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Cells J.E.,
RA Vandekerckhove J.,
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RT protein database of normal human epidermal keratinocytes.";
RL Electrophoresis 13:960-969(1992).
RN [5]
RN SEQUENCE OF 17-26 AND 93-103.
RC TISSUE=Erythrocyte;
RX MEDLINE-94147970; PubMed-8313871;
RX Golaz O., Hughes G.J., Frutiger S., Paquet N., Balroch A.,
RX Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RX Balant L., Hochrasser D.F.;
RT "Plasma and red blood cell protein maps: update 1993.";
RL Electrophoresis 14:1223-1231(1993).
RN [6]
RN SEQUENCE OF 17-26; 111-135 AND 140-157.
RC TISSUE=Colon carcinoma;
RX MEDLINE-97295306; PubMed-9150948;
RX Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -1- FUNCTION: REDUCES PEROXIDES WITH REDUCING EQUIVALENTS PROVIDED
CC THROUGH THE THIOREDOXIN SYSTEM. IT IS NOT ABLE TO RECEIVE
CC ELECTRONS FROM GLUTAREDOXIN. MAY PLAY AN IMPORTANT ROLE IN
CC ELIMINATING PEROXIDES GENERATED DURING METABOLISM. MIGHT
CC PARTICIPATE IN THE SIGNALING CASCADES OF GROWTH FACTORS AND TUMOR
CC NECROSIS FACTOR-ALPHA BY REGULATING THE INTRACELLULAR
CC CONCENTRATIONS OF H(2)O(2).
CC -1- FUNCTION: ENHANCES NATURAL KILLER (NK) CELLS ACTIVITY.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- PTM: THE CYS-51-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
CC H(2)O(2), AND THE OXIDIZED CYS-51 (PROBABLY CYS-SOH) RAPIDLY
CC REACTS WITH CYS-172-SH OF THE OTHER SUBUNIT TO FORM AN
CC INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
CC REDUCED BY THIOREDOXIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHC/TSA FAMILY.
CC -----
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CC -----
DR EMBL: 222548; CA80269.1;
DR EMBL: L19185; AA50465.1;
DR EMBL: X82321; CA57764.1;
DR HSSP: P30041; IPRX.
DR SWISS-2DPAGE: P32119; HUMAN.
DR Aarhus/Ghent-2DPAGE: 6116; IEF.
DR MIM: 600538;
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA.1.
KW Antioxidant.
FT ACT_SITE 51 51 BY SIMILARITY.
FT ACT_SITE 172 172 BY SIMILARITY.
FT CONFLICT 59 66 SNRADER -> TTVKRTSA (IN REF. 1).
FT CONFLICT 82 82 T -> N (IN REF. 2).
FT CONFLICT 105 105 A -> G (IN REF. 2).
FT CONFLICT 120 120 T -> N (IN REF. 1).
FT CONFLICT 175 175 G -> A (IN REF. 1).
FT CONFLICT 180 180 S -> R (IN REF. 1).
SQ SEQUENCE 198 AA; 21892 MW; 1AC781D908B32B46 CRC64;

Query Match 34.8%; Score 343.5; DB 1; Length 198;
Best Local Similarity 38.7%; Pred. No. 6.3e-24;
Matches 72; Conservative 38; Mismatches 67; Indels 9; Gaps 5;

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DR MGD: MGI:88034; Prdx3.
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA.1.
KW Antioxidant; Mitochondrion; Transist peptide.
FT TRANSIT 1 63 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 64 257 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
FT ACT_SITE 109 109 BY SIMILARITY.
FT ACT_SITE 230 230 BY SIMILARITY.
SQ SEQUENCE 257 AA; 28127 MW; 66513f2c5f1d56c0 CRC64;

Query Match 34.2%; Score 337.5; DB 1; Length 257;
Best Local Similarity 38.5%; Pred. No. 3e-23;
Matches 67; Conservative 35; Mismatches 67; Indels 5; Gaps 3;

QY 11 FKNQAFKNGEFTETKEDTGRMSVFFFPADFTFVCCTELGDVADHYEELQKLGVDY 70
DB 73 FKGTAIVNGEKEISLDDEKRYLV-LFEPYPLDFTFVCCTELIARSDKASEFHDVNCVY 131

QY 71 AVSTDTHTFKAMHSSSET---IAKIKYAMIDPTGALTRFNDNMRDEGLADRATFYVD 127
DB 132 AVSVSHFSLHAWINTPRKNGGIGHMNTLLSDITKQISRDYGLLEGSLRGLEFTID 191

QY 128 PGGITQALEVTAEIGGRDASDLIRKIKAAQYVASHPEGVCPAKMKEGEATLAP 181
DB 192 PNGVVKHLSVNDLPVGRSVEETLRVAKAQVEYETH-GEVCPANWTPESPTIKPS 244

RESULT 15
PDX3_BOVIN STANDARD; PRT; 257 AA.
AC P35705;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ThioRedoxin-dependent peroxidase, mitochondrial precursor
DE (Peroxiredoxin 3) (Antioxidant protein 1) (AOP-1) (SP-22 protein).
GN PROX3 OR AOP1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=97069947; PubMed=8912927;
RA Hiroi T., Watabe S., Takimoto K., Yago N., Yamamoto Y., Takahashi S.Y.,
"The cDNA sequence encoding bovine SP-22, a new defence system
against reactive oxygen species in mitochondria.";
DNA Seq. 6:239-242(1996).
[2]
RN [2]
RP SEQUENCE OF 2-257 FROM N.A.
RC TISSUE=Adrenal medulla;
RX MEDLINE=94373407; PubMed=8089078;
RA Watabe S., Kohno H., Kouyama H., Hiroi T., Yago N., Nakazawa T.,
"Purification and characterization of a substrate protein for
mitochondrial Atp-dependent protease in bovine adrenal cortex.";
J. Biochem. 115:648-654(1994).
CC -1- FUNCTION: THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE. PROTECTS
RADICAL-SENSITIVE ENZYMES FROM OXIDATIVE DAMAGE BY A RADICAL-
GENERATING SYSTEM.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED, UPON OXIDATION (BY
SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- PTM: THE CYS-109-SH GROUP IS THE PRIMARY SITE OF OXIDATION BY
H2(O)2, AND THE OXIDIZED CYS-109 (PROBABLY CYS-SOH) RAPIDLY
REACTS WITH CYS-230-SH OF THE OTHER SUBUNIT TO FORM AN
INTERMOLECULAR DISULFIDE. THIS DISULFIDE MIGHT SUBSEQUENTLY BE
REDUCED BY THIOREDOXIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D82025; BAA11511.1; -.
DR HSP: P30041; IPRX.
DR InterPro: IPR000866; Ahpc-TSA.
DR Pfam: PF00578; Ahpc-TSA.1.
KW Antioxidant; Mitochondrion; Transist peptide.
FT TRANSIT 1 63 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 64 257 THIOREDOXIN-DEPENDENT PEROXIDE REDUCTASE.
FT ACT_SITE 109 109 BY SIMILARITY.
FT ACT_SITE 230 230 BY SIMILARITY.
SQ SEQUENCE 257 AA; 28195 MW; F2B89EE2F172A42D CRC64;

Query Match 34.0%; Score 335.5; DB 1; Length 257;
Best Local Similarity 39.9%; Pred. No. 4.5e-23;
Matches 69; Conservative 33; Mismatches 66; Indels 5; Gaps 3;

QY 11 FKNQAFKNGEFTETKEDTGRMSVFFFPADFTFVCCTELGDVADHYEELQKLGVDY 70
DB 73 FKGTAIVNGEKEISLDDEKRYLV-LFEPYPLDFTFVCCTELIARSDKASEFHDVNCVY 131

QY 71 AVSTDTHTFKAMHSSSET---IAKIKYAMIDPTGALTRFNDNMRDEGLADRATFYVD 127
DB 132 AVSVSHFSLHAWINTPRKNGGIGHMNTLLSDITKQISRDYGLLEGSLRGLEFTID 191

QY 128 PGGITQALEVTAEIGGRDASDLIRKIKAAQYVASHPEGVCPAKMKEGEATLAP 180
DB 192 PNGVVKHLSVNDLPVGRSVEETLRVAKAQVEYETH-GEVCPANWTPESPTIKPS 243

Search completed: May 19, 2002, 01:58:37
Job time: 5236 sec

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DB 1 MSLINTEIRPFAQAKDGRFVTSADVADYKGSV-FFFPADFTFVCPTELEDLADNDY 59
QY 61 ELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTRFNDMRDEGLAD 120
DB 60 VETRLGVEIYAVSTDTHTFKAMHSDSPAIGKIKYTMVGPSPGOVNFNFEIMRPGVOLAD 119
QY 121 RAEFVVDPOGIIQAEVTAEGIGRDSADLRKIKAAQYVASHGECVPAKKEGEATLAP 180
DB 120 RGTFLVDPOGVIOFMETVABEGIRNAIELLRKIKAAQYVAHNGEVCAPAKKEGEATLAP 179
QY 181 SLDLVGKI 188
DB 180 SLDLVGKI 187

RESULT 2
ID 082863 PRELIMINARY; PRT; 187 AA.
AC 082863;
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 17, Last annotation update)
DE AHPC.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOL;
RA Fukumori F., Horikoshi K.;
RT "Toluene induced Constitutive Overexpression of An Alkyl Hydroperoxide
RT Reductase Small Subunit in Pseudomonas putida: Molecular Cloning of
RT the ahp genes.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB010689; BAA31468.1; -.
DR HSSP; P30041; 1PRX.
DR InterPro; IPR000866; Ahpc-TSA.
DR Pfam; PF00578; Ahpc-TSA; 1.
SQ SEQUENCE 187 AA; 20507 MW; CC6351406B9C8168 CRC64;
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Query Match 72.9%; Score 719.5; DB 2; Length 187;
Best Local Similarity 67.6%; Pred. No. 7.3e-59;
Matches 127; Conservative 34; Mismatches 26; Indels 1; Gaps 1;

QY 1 MSLINTEIRPFAQAKDGRFVTSADVADYKGSV-FFFPADFTFVCPTELEDLADNDY 59
DB 1 MSLINTEIRPFAQAKDGRFVTSADVADYKGSV-FFFPADFTFVCPTELEDLADNDY 59
QY 61 ELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTRFNDMRDEGLAD 120
DB 60 EFKKLGVEIYAVSTDTHTFKAMHSDSPAIGKIKYTMVGPSPGOVNFNFEIMRPGVOLAD 119
QY 121 RAEFVVDPOGIIQAEVTAEGIGRDSADLRKIKAAQYVASHGECVPAKKEGEATLAP 180
DB 120 RGTFLVDPOGVIOFMETVABEGIRNAIELLRKIKAAQYVAHNGEVCAPAKKEGEATLAP 179
QY 181 SLDLVGKI 188
DB 180 SLDLVGKI 187
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RESULT 3
ID 09PD49 PRELIMINARY; PRT; 206 AA.
AC 09PD49;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SUBUNIT C OF ALKYL HYDROPEROXIDE REDUCTASE.
```

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GN XF1530.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Aencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carriero D.M., Carier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Fromme M., Furlan L.R.,
RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E.Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terezi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Zeldanis J., Zetubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE003983; AAF84339.1; -.
DR HSSP; P30041; 1PRX.
KW Complete proteome.
SQ SEQUENCE 206 AA; 22891 MW; AF703BDE833698D6 CRC64;
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Query Match 72.3%; Score 714; DB 16; Length 206;
Best Local Similarity 69.1%; Pred. No. 2.7e-58;
Matches 130; Conservative 29; Mismatches 27; Indels 2; Gaps 2;

QY 1 MSLINTEIRPFAQAKDGRFVTSADVADYKGSV-FFFPADFTFVCPTELEDLADNDY 59
DB 21 MSVINTELSKRAYKNGQVEVSEAVLKGKAV-FFFPADFTFVCPTELEDLADNDY 79
QY 61 ELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTRFNDMRDEGLAD 120
DB 80 EFKKLGVEIYAVSTDTHTFKAMHSDSPAIGKIKYAMIGDPTGALTRFNDMRDEGLAD 138
QY 121 RAEFVVDPOGIIQAEVTAEGIGRDSADLRKIKAAQYVASHGECVPAKKEGEATLAP 180
DB 139 RGTFLVDPOGVIOFMETVABEGIRNAIELLRKIKAAQYVAHNGEVCAPAKKEGEATLAP 179
QY 181 SLDLVGKI 188
DB 199 SLDLVGKI 206
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RESULT 4
ID 09KH10 PRELIMINARY; PRT; 187 AA.
AC 09KH10;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PEROXIREDOXIN.
```

OS *Thermus aquaticus*.
OC *Bacteria*; *Thermus*/*Deinococcus* group; *Thermus* group; *Thermus*.
OX NCBI_TaxID:271;
RN [1]
RP
SEQUENCE FROM N.A.
RX MEDLINE=20459059; PubMed=10862622;
RA Logan C., Mayhew S.G.;
RT "Cloning, overexpression, and characterization of peroxiredoxin and
RT NADH peroxiredoxin reductase from *Thermus aquaticus*.";
RL J. Biol. Chem. 275:30019-30028(2000).
DR EMBL: AF276071; AAF82118.1; -
SQ SEQUENCE 187 AA; 20982 MW; F4D33C459D104819 CXC6;

Query Match	69.7%;	Score 687.5;	DB 2;	Length 187;
Best Local Similarity	65.4%;	Pred. NO.	6.8e-56;	
Matches 123;	Conservative 32;	Mismatches 33;	Indels 1;	Gaps 1;
<hr/>				
QY	1	MSLINTKIKPRKNQAFKNGEFLTEIKDETKGRMWSVEFFFYPADFTFCVCTELGDVAADHAE	60	
		: : : : : : : :		:
b	1	MSLVGKKKQPRAQAQYHNHGEELEVEEDOPMGKWSI-VCFYPADFVFVCCTELEDDODHYA	59	
<hr/>				
QY	61	ELOKGVNVAVVSPTDHTFTHKAMHSSSTIAKIKAKMGDPGATLTRNDNRREDEGLAD	120	
	::: :	:: : : : :		
.Db	60	TFKELGEVSVSDTHTHKAMHDTSPIAISLEYVMIGDPSHQSRMDVDVLDDEOGLAQ	119	
<hr/>				
QY	121	RATEVPEOGITIOALEVTAEGISGRDASDLRLRIKAQAQVVASHPGEVCPAKMKKEGETLAP	180	
	:	: : : : : : :		
.Db	120	RGTFIIDPDGYIQAVEINADGIGRNASTLIDRIKAQAQYVRNHPGEVCPAKMKMEGAETLKRP	179	
<hr/>				
QY	181	SLLDVGKI	188	
.Db	180	SLLDVGKI	187	

RESULT	5			
087200				
ID	087200	PRELIMINARY:	PRT:	168 AA.
AC	087200;			
DT	01-NOV-1998 (TREMBLrel. 08.	Created)		
DT	01-NOV-1998 (TREMBLrel. 08.	Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19.	Last annotation update)		
DE	ALKYL HYDROPEROXIDE REDUCTASE C.			
GN	AHPC.			
OS	Amphibacillus xylanus.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
OC	Bacillus/Staphylococcus group; Amphibacillus.			
OX	NCBI_Taxid=1449;			
IN	[1]			
RP	SEQUENCE FROM N.A.			
RP	STRAIN-EP01;			
RA	MEDLINE=20416213; PubMed=10960086;			
RA	Nimura Y., Nishiyama Y., Saito D., Tsuji H., Hidaka M., Miyaji T.,			
RA	Watanabe T., Massey V.;			
RT	"A Hydrogen Peroxide-Forming NADH Oxidase That Functions as an Alkyl			
RT	Hydroperoxide Reductase in Amphibacillus xylanus.";			
RL	J. Bacteriol. 182:5046-5051(2000).			
DR	EMBL: AB016435; BAA33808.1; -			
DR	InterPro: IPR000866; AHPC-TSA.			
DR	Pfam: PF00578; AHPC-TSA.1.			
QO	SEQUENCE 188 AA; 20774 MW; E61BA53C0215BA84 CRC64;			

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Query Match      67.1% Score 662; DB 2; Length 188;
Best Local Similarity    63.0%; Pred. No. 1.6e-53;
Matches   119; Conservative   33; Mismatches   35; Indels     2; Gaps     2.
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QY 1 MSLLNTKIKIPKNAQFKNG-EFIEITKEDTEGRMSVFEFFFYPADETFVCPTELGVADHY 59
||||| :|||: ||||: |::|:| :|||: |||||:||||| ||
DB 1 MSLLCTEVPFAAQFGSKNDFEEVTLEADKKWSI-VVEFYADPSFVCPTELEVDKEY 59
||:|||||:|||:||||| ||||| :|||:||||| :||| :|||

OY 60 EELQKLSTGVAVSDTHFTKRAMSSSETLAKIKYIMGPTGALTRFNEDNMREDECIA 119
||:|||||:|||:||||| ||||| :|||:||||| :||| :|||

Db 60 AELKRLGEVYVSVDTHFVHKAKHENSAPVSGTIEYIMIGDSQTIISRFVDLNEEFGLA 119

QY 120 DRAFEVVDPOSTIOAIEFTVTAEGTIGRDSADLIRKIAAOYVASHGECVPPMKKRGATLA 179

Db 120 DRGFIIIDPDGVIOAIEFINMDGIGRDSATLIRKIAAOYVRENFBVCPPAKMEGSGFTLK 179

QY 180 PSLDLVGI 188

Db 180 PSLDIVGI 188

RESULT	6			
053647				
ID	053647	PRELIMINARY:	PTT:	189 AA.
AC	053647			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C (Ec 1.6.4.-).			
GN	AHPC OR SA0366 OR SAV0381.			
OS	Staphylococcus aureus,			
OS	Staphylococcus aureus (strain N315), and			
OS	Staphylococcus aureus (strain Mu50).			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;			
CC	Bacillus/Staphylococcus group; Staphylococcus.			
OX	NCBI_TaxID=1280, 158879, 158878;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=S.aureus; STRAIN=RN4220;			
RC	MEDLINE=96004465; PubMed=7551034;			
RA	Amlstrong-Buisseret L., Cole M.B., Stewart G.S.;			
RT	"A homologue to the Escherichia coli alkyl hydroperoxide reductase			
RT	Ahpc is induced by osmotic upshock in Staphylococcus aureus."			
RL	Microbiology 141:1655-1661(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=S.aureus; STRAIN=RN4220;			
RA	Jones E.C., Francis K.P., Stewart G.S.A.B.;			
RL	Submitted (MAR-1997) to the EMBL/Genbank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);			
RC	MEDLINE=91311952; PubMed=11418146;			
RA	Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,			
RA	Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,			
RA	Kanamori M., Matsumaru H., Matuyama A., Murakami H., Hosoyama A.,			
RA	Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,			
RA	Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,			
RA	Keneshima M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T			
RA	Hattori M., Ogasawara N., Haysashi H., Hiramatsu K.;			
RT	"Whole genome sequencing of methicillin-resistant Staphylococcus			
RT	aureus."			
RL	Lancet 357:1225-1240(2001).			
CC	-1- FUNCTION: DIRECTLY REDUCES ORGANIC HYDROPEROXIDES IN ITS REDUCED			
CC	DITHIOL FORM (BY SIMILARITY).			
CC	-1- INDUCTION: BY OSMOTIC UPSHOCK.			
CC	-1- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY.			
DR	EMBL: U92441; AAB5151.1; -			
DR	EMBL: AP003130; BAB1593.1; -			
DR	EMBL: AP003359; BAB56543.1; -			
DR	EMBL: IPR000866; Ahpc-TSA.			
DR	Pfam: pf00578; Ahpc-TSA; 1.			
DR	Oxidoreductase; Complete proteome			
SO	SEQUENCE 189 AA; 20976 MW; P/13449C8406B73 CRC64;			

Query Match 65.3%; Score 64.5; DB 16; Length 169;
Best Local Similarity 64.2%; Pred. No. 6, 6e-52;
Matches 122; Conservative 25; Mismatches 40; Indels 3; Gaps 2

OY 1 MSLLTKTKPKRNQAF--KNGEFFITEKDTGRRSVFFFPADFTVCPPELGDVADH 58
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
db 1 MSLLKEILPTPAQAQFDRKKDQFKVTQEDDLGNSVV--VCFFPADPSPFCPELELDNQ 59
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 59 YEELQKLGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTNRDNKREDEGL 118
DB 60 YEELQKLGVDYAVSTDTHTFKAMHSDAISKITTYTMIGDPSQITTRNDVDEATGL 119
QY 119 ADRAITFVVDPOGIIQAEIVTAEGIGRSDASDLRKIKAAQYVASHPEGVCAPAKWKEGATL 178
DB 120 AQRGTFTIIDPGVQASEINADGIGRDSATLAKRIKAAQYVRKNPGEVCPAKWKEGAKTL 179
QY 179 APSLDLVGKI 188
DB 180 QPGLDLVGKI 189

RESULT 7
Q9R072 PRELIMINARY; PRT; 188 AA.
ID 09R072:
AC 09R072:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
E ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT C.
GN AHPC.
OS Bacteroides fragilis.
OC Bacteria; CFB group; Bacteroidetes; Bacteroidales; Bacteroidaceae;
OC Bacteroides.
OX NCBI_TaxID=817;
RN SEQUENCE FROM N.A.
RP STRAIN=638R.
RC MEDLINE=99412269; PubMed=10482511;
RA Rocha E.R., Smith C.J.;
RT Role of the alkyl hydroperoxide reductase (ahpc) gene in oxidative
RT stress defense of the obligate anaerobe Bacteroides fragilis.*;
RL J. Bacteriol. 181:5701-5710(1999).
DR EMBL; AF129406; AAD52147.1; -.
DR InterPro: IPR000866; Ahpc-TSA.
DR pfam: PR00578; Ahpc-TSA; 1.
SQ SEQUENCE 188 AA; 21061 MW; 4A474FF66D6C614 CRC64;

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Query Match 64.0%; Score 631.5; DB 2; Length 188;
Best Local Similarity 60.8%; Pred. No. 1e-50;
Matches 113; Conservative 38; Mismatches 34; Indels 1; Gaps 1;

QY 3 LINTKIKPFKNQAFKNGEFLITEKDTGRMSVFFFPADTFVCPTELGDVADHYEEL 62
DB 4 IINSQMEFEVQAFQNGSFVTSSEDDKGMAL-FFFPADTFVCPTELGDVADHYEEL 62
DB 63 QKIGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTNRDNKREDEGLADRA 122
DB 63 QAMGVEVYVSTDSHFVHKAMHSDAISIRIKYPMADPTGILSRGVMIEEGMAYRG 122
QY 123 TFVVDPOGIIQAEIVTAEGIGRSDASDLRKIKAAQYVASHPEGVCAPAKWKEGATLAPSL 182
DB 123 TELVNEBGRKKAIEIDNNIGRNADELKRVKAAQYVATHDGEVCPAKWKEGATLPST 182
QY 183 DLVGKI 188
DB 183 DLVGKI 188

RESULT 8
Q99XR7 PRELIMINARY; PRT; 186 AA.
ID 099XR7:
AC 099XR7:
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE ALKYL HYDROPEROXIDASE.
GN AHPC OR SPY2079.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

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OC Streptococcus.
OX NCBI_TaxID=1314;
RN 111:
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006628; AK34732.1; -.
DR Peroxidase; Complete proteome.
SQ SEQUENCE 186 AA; 20483 MW; 5B7147A476DBAEP1 CRC64;

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Query Match 63.7%; Score 629; DB 16; Length 186;
Best Local Similarity 62.2%; Pred. No. 1.8e-50;
Matches 117; Conservative 28; Mismatches 41; Indels 2; Gaps 2;

QY 1 MSLINTKIKPFKNQAFKNGEFLITEKDTGRMSVFFFPADTFVCPTELGDVADHYE 60
DB 1 MSLIGKEIAEFSQAQYHDGKFTVTNEDVKGMAV-FCFPADTFVCPTELGDLOEQYE 59
QY 61 ELQKIGVDYAVSTDTHTFKAMHSSSETIAKIKYAMIGDPTGALTNRDNKREDEGLAD 120
DB 60 TLKSLGVEVYVSTDTHTFKAMHSDSDVGTITYPHIGDPSHLISQAFVLGSD-GLAQ 118
QY 121 RAFTVVDPOGIIQAEIVTAEGIGRSDASDLRKIKAAQYVASHPEGVCAPAKWKEGATLAP 180
DB 119 RGTFIVDPDGIQAMETINADGIGRDSATLIDKIHAAQYVRKNPGEVCPAKWKEGATLTP 178
QY 181 SLDLVGKI 188
DB 179 SLDLVGKI 186

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RESULT 9
ID 066265 PRELIMINARY; PRT; 186 AA.
AC 066265:
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ALKYL HYDROPEROXIDASE.
GN AHPC.
OS Streptococcus mutans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1309;
RN SEQUENCE FROM N.A.
RP STRAIN=NCIB 11723;
RC MEDLINE=20120090; PubMed=10656297;
RA Poole L.B., Higuchi M., Shimada M., Li Calzi M., Kamio Y.;
RT "Streptococcus mutans H202-forming NADH oxidase is an alkyl
RT hydroperoxide reductase protein.";
RL Free Radic. Biol. Med. 28:108-120(2000).
RN 121:
RP SEQUENCE FROM N.A.
RC STRAIN=NCIB 11723;
RX MEDLINE=95036869; PubMed=7765479;
RA Higuchi M., Shimada M., Matsumoto J., Yamamoto Y., Rhaman A.,
RA Kamio Y.;
RT "Molecular cloning and sequence analysis of the gene encoding the
RT H202-forming NADH oxidase from Streptococcus mutans.";
RL Biosci. Biotechnol. Biochem. 58:1603-1607(1994).
DR EMBL; AB010712; BAA25695.1; -.
DR InterPro: IPR000866; Ahpc-TSA.
DR pfam: PR00578; Ahpc-TSA; 1.
DR Peroxidase.
SQ SEQUENCE 186 AA; 20478 MW; 1C7E9BEA4D739F06 CRC64;

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RL J. Bacteriol. 179:3944-3949(1997).
 DR EMBL: U94336; AAC45425.1; -
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 SQ SEQUENCE 187 AA; 20462 MW; 844A58ABC4E6AC4 CRC64;

Query Match 59.7%; Score 589.5; DB 2; Length 187;
 Best Local Similarity 56.9%; Pred. No. 8.1e-47;
 Matches 107; Conservative 33; Mismatches 47; Indels 1; Gaps 1;

QY 1 MSLLNTRKIPKRNQAFKNGEIEITEKDTGGRMSVFFFFYPADFTVCPTLGDVADHYE 60
 DB 1 MSLLNTRKIPKRNQAFKNGEIEITEKDTGGRMSVFFFFYPADFTVCPTLGDVADHYE 60
 QY 61 ELQKLGVDVAVSTDTHTFHKAHSSSETIAKIKYAMIGDPTGALTRFDMRDEGLAD 120
 DB 60 AFQKAGAEVYIVTDTHTSHKVMHETSFAVGKAOFPPLIGDPTHKLTAFGVHIEEGLAL 119
 QY 121 RATFVVDPGIIOAIEVTAGSIGDASDLRKIRAAQYVASHPEVCPAKWKEGEATLAP 180
 DB 120 RGTFLINEGVYIKTLEIHDSIARDVETETKLTAAQGVANNPQYCPAKWKEGEATLAP 179
 QY 181 SLDLVGKI 188
 DB 180 SLDLVGKI 187

RESULT 13
 ID 030738 PRELIMINARY; PRT; 187 AA.
 AC 030738;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ALKYL HYDROGEN PEROXIDE REDUCTASE.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JH2-7;
 RX MEDLINE=98117057; PubMed=9457879;
 RA Rice L.B., Carlas L.L.;
 RT Transfer of Tn385, a composite, multiresistance chromosomal element from Enterococcus faecalis.*
 RL J. Bacteriol. 180:714-721(1998).
 EMBL: AF016233; AAC46081.1; -
 HSSP: P30041; 1PRX.
 DR InterPro: IPR000866; Ahpc-TSA.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN.1.
 SQ SEQUENCE 187 AA; 21090 MW; C400392C7CB98487 CRC64;

Query Match 57.1%; Score 563.5; DB 2; Length 187;
 Best Local Similarity 54.3%; Pred. No. 2.1e-44;
 Matches 102; Conservative 39; Mismatches 46; Indels 1; Gaps 1;

QY 1 MSLLNTRKIPKRNQAFKNGEIEITEKDTGGRMSVFFFFYPADFTVCPTLGDVADHYE 60
 DB 1 MSLLNTRKIPKRNQAFKNGEIEITEKDTGGRMSVFFFFYPADFTVCPTLGDVADHYE 59
 QY 61 ELQKLGVDVAVSTDTHTFHKAHSSSETIAKIKYAMIGDPTGALTRFDMRDEGLAD 120
 DB 60 HLOELNCEVYSSVSDSHYHKKAMADATETIKTKYPMADPNQOLRFEGVLDASGMAY 119
 QY 121 RATFVVDPGIIOAIEVTAGSIGDASDLRKIRAAQYVASHPEVCPAKWKEGEATLAP 180
 DB 120 RASFVSPBGDIKSYEINDMIGIRNAEELVRKLEASQFAEHODKVCAPNMWQGEETIAP 179

QY 181 SLDLVGKI 188
 DB 180 SLDLVGKI 187

RESULT 14
 ID 083522 PRELIMINARY; PRT; 188 AA.
 AC 083522;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ALKYL HYDROPEROXIDE REDUCTASE (AHPc).
 GN TP0509.
 OS Treponema pallidum
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID=160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLES;
 RX MEDLINE=98332770; PubMed=9665876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
 RA McDonald L., Artlich P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RT "Complete genome sequence of Treponema pallidum, the syphilis
 spirochete.";
 RL Science 281:375-388(1998).
 DR EMBL: AE001227; AAC65497.1; -
 DR HSSP: P30041; 1PRX.
 DR TIGR: TP0509;
 DR InterPro: IPR000866; Ahpc-TSA.
 DR Pfam: PF00578; Ahpc-TSA; 1.
 KW Complete proteome.
 SQ SEQUENCE 188 AA; 20709 MW; 44D2CFDPA3420AFE CRC64;

Query Match 49.5%; Score 488.5; DB 16; Length 188;
 Best Local Similarity 49.7%; Pred. No. 1.8e-37;
 Matches 93; Conservative 32; Mismatches 61; Indels 1; Gaps 1;

QY 2 SLNTRKIPKRNQAFKNGEIEITEKDTGGRMSVFFFFYPADFTVCPTLGDVADHYE 61
 DB 3 SLNTRKIPKRNQAFKNGEIEITEKDTGGRMSVFFFFYPADFTVCPTLGDVADHYE 61
 QY 62 LQKLGVDVAVSTDTHTFHKAHSSSETIAKIKYAMIGDPTGALTRFDMRDEGLAD 121
 DB 62 FVEIGCKVYSSVSDSHYHKKAMADATETIKTKYPMADPNQOLRFEGVLDASGMAY 121
 QY 122 RATFVVDPGIIOAIEVTAGSIGDASDLRKIRAAQYVASHPEVCPAKWKEGEATLAP 181
 DB 122 GTFVVDPEGLVKAFAEVDHMGIGRDADELRLKYOSQFAVAKHGDQVPAKWKGEATLAP 181
 QY 182 SLDLVGKI 188
 DB 182 SLDLVGKI 188

RESULT 15
 ID 066779 PRELIMINARY; PRT; 211 AA.
 AC 066779;
 DT 01-AUG-1998 (TREMblrel. 07, Created)
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ALKYL HYDROPEROXIDE REDUCTASE.
 GN AHPc1 OR AQ_486.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificales; Aquificaceae; Aquifex.
 OX NCBI_TaxID=63363;

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